SMACHE: Space-efficient Caching for Self-Similar Data

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1. Introduction

Scientific applications are on the verge of generating enough data to overwhelm existing computing paradigms. For example, next generation sequencing technology from Applied Biosystems, SOLiD, generates approximately 1 terabyte of image data every run [1]. In this magnitude, data rapidly overwhelms any individual system and must be processed by a distributed system. We have built a space-efficient caching mechanism that can be used by next-generation distributed systems that grapple with the problem of "big data".

Manually managing and distributing data to a distributed application is often too complex and burdensome for a programmer. New programming frameworks such as Map-Reduce reverse the relationship between data and computation on a cluster. Instead of moving data to a processing element, logic and computation move to the data and execute where it resides.

Unfortunately, long-lived computations may require several pieces of data simultaneously and it may not be possible to schedule a computation near everything it needs. For example, it may not be possible to schedule an application that compares the genome from human A and the genome from human B on a node where both genomes are available. Thus, even a data-centric paradigm such as Map-Reduce does not completely eliminate the need to move data.

We believe that SnowFlock [7] is a useful paradigm for simplifying cluster computing. SnowFlock allows programmers to fork Virtual Machine (VM) instances to create new compute instances. New VMs may still be scheduled and moved near data in order to minimize the cost of accessing the large data sets that the program needs. In SnowFlock however, more flexibility is given to the programmer.

In general, both data-centric paradigms such as Map-Reduce and hybrid paradigms such as SnowFlock require efficient data *and* computation transport. We can we reduce (but not eliminate) the amount of data that must moved by moving some of the compute logic. VM data and biological data have much more in common than it would seem at a cursory glance; both are simply program specifications[1]. Both share the same tendency to have internal repetition and self-similarity as well as similarity to other biological data or VM images. For example: similar snippets of code and data frequently repeat in both genomes [8] and different programs on a disk. Similarly, genomes from different members of the same species are largely similar with only small mutations just as different versions of a Debian disk image are similar.

We provide space-efficient caching of data exhibiting high-levels of self-similarity by using content-addressable storage and content-sensitive block algorithms. These techniques have previously been applied to *significantly* reduce the amount of data required to synchronize large collections of files over a network [11, 10], but they also have applicability for maintaining efficient caches on disk or in memory. These caches would similarly allow for efficient data replication across the network. In both SnowFlock and paradigms such as Map-Reduce, caching is necessarily used to ensure that the costs of transferring data and computation between nodes is minimized.

[1] A humorous bit of oversimplification.

2. Insight and Approach

Several protocols exist for efficiently transferring data from a remote site when *partial* information already exists locally. A famous example of such a protocol is `rsync` [12]. Whilst `rsync` is dependent on specific files, protocols such as remote differential compression [11] (RDC) leverage the fact that several files may contain similar data or that names may have changed.

We use techniques similar to those employed by RDC in order to efficiently *store* data exhibiting self-similarity. We exploit two fundamental techniques: content-addressable storage and content-sensitive block algorithms. A brief overview of these techniques is included here.

Content-Addressable Storage

Content-addressable storage is a general scheme of addressing and storing data. Instead of using identifiers such as filenames, data is identified by some function of its content. Thus, if two pieces of data are identical then they are treated as the same. E.g., if two files have the same contents, content-addressable storage will consider them to be same entity and store the data only once.

SMACHE uses cryptographic hashes to derive an identifier for data. Instead of a filename, data is identified by a hash of its contents. In general, if storage data chunks are limited in size, then larger data can be represented as a sequence of identifiers for smaller chunks. This is discussed in further detail in Section 3.

By dividing and storing data in such a way, redundancy can be minimized. For example, if two files are largely similar, then many data blocks they contain will be the same, and their sequences of identifiers may be largely similar. Each of the chunks shared by these two files need only be stored once. Such a system does have drawbacks: if files are largely unique, then hashes and sequences of identifiers impose an overhead both in space and in time – since a file is no longer stored sequentially it may take longer to access.

Content-Sensitive Block Algorithms

When storing a large chunk of data, a block algorithm is employed to divide it up into smaller, more manageable pieces. A content-sensitive block algorithm is a mechanism used for dividing data into blocks, that minimizes the number of blocks that change when a small amount of the underlying data changes.

This is useful in the context of a content-addressable storage system. Consider making changes to a file which is stored in such a system. If a small amount of data in the file changes, we would like to store as few new content-addressed blocks as possible, and simply refer to blocks already stored. A content-sensitive block algorithm may be used to divide the data into chunks in both the

original and new file, in order to ensure that as many blocks as possible are repeated and thus already stored.

To divide data into chunks, a block algorithm selects appropriate cut points within a data stream. For example, a fixed-size block algorithm may select a cut point every 512 bytes. Such an algorithm does not minimize the number of blocks that change when the underlying data changes, however. If a single byte is inserted at the beginning of the data, then every single block will be slightly different than in the first case.

A content-sensitive block algorithm uses the data itself to determine where cut points should be made. For example, every time a sequence of bytes with value `0xdeadbeef` in seen in the data, a cut point may be defined. Thus if a single byte is inserted at the beginning of the data, only the first block will be changed. In reality, no a priori distribution of content is assumed. Content-sensitive block algorithms are generally run over a sequence generated by taking a hash over a window in the original data, such as a Rabin-Karp hash [6], in order to ensure that the data is uniformly distributed.

SMACHE uses a Rabin-Karp hash over a window of size 32 to perform content-sensitive blocking. A cut point is defined whenever the resulting stream has a value which is zero modulus the desired mean block size. Generally, we use 512 as the mean block size.

Goals

By storing only unique blocks and sending data as sequences of hashes, SMACHE intends to achieve significant savings for data that exhibits a high-degree of self-similarity while still remaining general-purpose.

Biological data shows a high degree of self similarity, which has been used effectively to compress far beyond 2 bits per base-pair [8]. Such similarity may come from shared genes or even common subsequences within a single genome such as promoters. Similar techniques have been applied to running VMs, which also exhibit high degrees of self-similarity, primarily for the purpose of fitting more running VMs into a smaller amount of memory [5].

The aim of this project is to provide speed on par with or faster than standard compression techniques such as Lempel-Ziv, with random access semantics, unlike Lempel-Ziv. We do not expect to beat compression ratios achieved by standard compression algorithms, however we do expect to see significant gains over an uncompressed cache.

This caching system can be used in two practical scenarios. First, on a cluster where the goal is to reduce the time to access data as much as possible. In this case, the bottleneck might be disk access; SMACHE may store its cache database in a distributed-memory system such as memcached [3]. Second, if the network bandwidth or latency is a limiting factor. This might be the case if a VM or dataset is remote; SMACHE may use a local backing store such as BerkeleyDB [9].

We believe that there is an attractive opportunity to compress biological data for caching purposes. Often in theoretical treatments of compression of biological data, performance is explicitly not given any regard [4]. However, no gains may be made by compression techniques if the computation cost is so high that data is generated faster than data can be compressed. The proposed technique should impose only moderate overhead. We intend it to be used for building *real systems*.

Additionally, we hope to take advantage of the similarity *between* sequences and VM images for gains in space-efficiency, something which is often not done in practice. The possible gains of zipping a single VM image or biological sequence are severely limited compared to those that can be made by compressing a set together. The reason that this does not happen using existing compression algorithm algorithms is because they often do not offer random access semantics, i.e. if one compresses ten sequences together then it is often necessary to extract all ten before extracting the last one. This is simply due to the nature of many compression algorithms.

3. Implementation

This intent of this project is to construct a useful building block on which future cloud computing tools and infrastructure may be based. In this Section, we describe some details of our system.

We implemented our system using `C` and `python` with a BerkeleyDB backend. Our implementation is extensible however, and it is quite trivial to add support for a `memcached` backend if the goal is a distributed cache.

The internals were implemented using `C` for performance and a `python` interface was developed for quick development of shell tools and test scripts. The `C` component is available as a shared library, `libsmache`, and is responsible for all hashing, block algorithms, searching and all interfacing with the backend. The `python` interface simply provides a means to ask the library to read and write files and data to the cache.

Several tools were developed in `python`. First, `smachezip` is a tool which allows for the creation and extraction of SMACHE caches. Second, `smachestats` is a tool which analyzes caches and extracts statistics; this was used for the generation of all graphs below. Finally, we built a daemon, `smachefs`, that exposes a SMACHE cache as a file system via FUSE [2].

3.1 Data Representation and Fetching

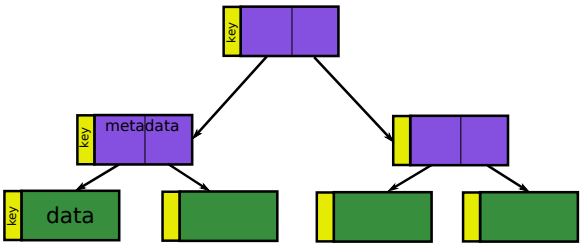


Figure 1. Example of how data is chunked and stored inside a SMACHE cache.

Before detailing algorithms, we describe how data is represented by SMACHE. All data in a SMACHE cache is uniquely identified by a single 16-byte hash value. This is known as the **key**. Complete files and small data chunks are not differentiated.

All data chunks stored in a backend by SMACHE are less than 64Kb. In order to store data larger than this size, SMACHE automatically generates **metadata** chunks – data chunks which contain lists of keys instead of actual data. Data is thus stored in a simple hierarchy, as illustrated in Figure 1. When retrieving the data associated with a metadata key, SMACHE transparently traverses this tree and does not require the user of the library to have any knowledge of metadata. For example, the data contained in all four leaf nodes in Figure 1 is uniquely identified by the key of the root node. The user need only pass in this key, a length and an offset to in order to read from the cache. Access semantics are still effectively random, since each metadata chunk may describe thousands of keys, not just two as depicted above for simplicity. In reality, the trees are very, very shallow. Data would have to be several terabytes before requiring more than a few levels.

Each block in a SMACHE cache has a reference count associated with it. This reference count is equal to the number of metadata blocks which refer to it (note that metadata blocks can refer to other metadata blocks). Keys that are returned to the user of the

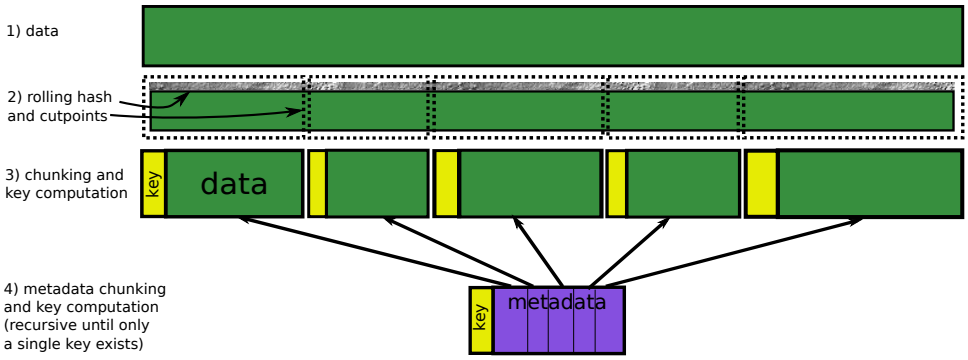


Figure 2. The algorithm used for storing data.

library (e.g., when inserting a file) are given a reference count of 1. The library provides facilities for manipulating these counts and automatically cleans up orphans.

```
D21DB157405AA29E760B51B67B3C1477 M_musculus/mm_ref_chr16.fa
76780C7295DD9144DCECC7D3FD238904 M_musculus/mm_ref_chr11.fa
B3AFCF056DB76AF0CC8D459A1B208537 M_musculus/mm_ref_chr10.fa
9E7D6046578135F121F2ABCB7E12156D M_musculus/mm_ref_chr15.fa
                    :
                    .
C1E58171F9A4B0E9040D17D70CB90436 M_musculus/mm_ref_chr06.fa
326AE42BCA5190BD884F1685AA5868CB M_musculus/mm_ref_chr13.fa
49265721AC201C7EE44462008F4AF7BD M_musculus/mm_ref_chr12.fa
9F1B6F170566BB9F053BF5765D8774EA M_musculus/mm_ref_chr03.fa
```

Figure 3. An index for a SMACHE cache containing a Mouse genome.

Since all data is uniquely identified only by a hash, the python tools that manipulate files (such as `smachezip`) have a simple mechanism for maintaining a mapping, known as the index, from a filename to a particular hash (and set of metadata for that file, such as ownership, permissions and modification times). Figure 3 shows a sample index file for a cache containing a genome of the common mouse. Such a mapping is similar to the mapping from a filename to a disk block or inode number.

3.2 Cache Insertion

This Section describes the process of inserting data into a SMACHE cache, as illustrated in Figure 2. The first step is to divide the data into blocks using a block algorithm. SMACHE supports using either Rabin-Karp hashes with a specified mean block size as described in Section 2 or fixed-size chunks. Once the data is divided into blocks, a key for each block is computing using an MD5 cryptographic hash. Before insertion, each data block is compressed using a simple algorithm based on Huffman coding; blocks are not compressed if there are no savings. This algorithm is better suited than a dictionary-based approach such as Lempel-Ziv, since the blocks are generally quite small. The compression aims only to save space when data consists of all readable ASCII characters, for example. Finally, a sequence of all keys describing the data is generated and this data is recursively inserted to the cache. When a single key may be used to describe the data, this key is returned to the user. The python tools use this single key as the identifier for the file in the index.

4. Evaluation

We evaluate the disk usage of SMACHE compared to uncompressed data and data that has been compressed with `gzip`. Note that we do not generally expect to perform better than `gzip`, since SMACHE is able to provide random access semantics; the inability to access random at arbitrary positions within the stream makes `gzip` inappropriate for caching.

We break down the disk usage of SMACHE into four components. First, there is the **data** itself. This is space occupied by data from the original stream, possibly slightly compressed as described in Section 3 Second, there are **keys**; this is the amount of data used to store all keys for data and metadata. Third, there is overhead associated with the storage of the **metadata** itself. Recall, the metadata consists of lists of the keys that make up a chunk of large data. Metadata chunks may be shared in the same way regular data chunks are shared. Finally, there is overhead used by the database backend, referred to as **DB overhead**. This overhead is related to data management structures employed by the database on disk, and in a real system could be reduced enormously and nearly eliminated (and our data management requirements are very simple). As described above, our implementation uses BekerleyDB [9] to store data, which demonstrated significant data overhead.

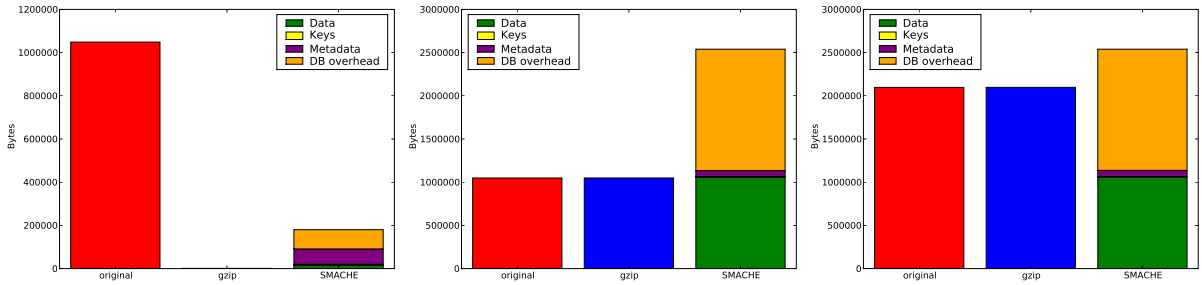
In this Section, we first test SMACHE on simple synthetic data to validate our algorithms and provide a frame of reference. Then, we evaluate its performance on a set of biological data, consisting of a few complete genomes. Finally, we test its performance in storing VM images.

4.1 Synthetic Data

In order to establish that SMACHE does it what claims, we first choose a simple set of synthetic benchmarks to cache. We used `smachezip` to compress one megabyte of all zeros, one megabyte of random data (uncompressable), and the same random data concatenated with a slightly modified copy of itself.

Figure 4 shows the performance of SMACHE on these three data sets relative to the original (uncompressed) data and data compressed with `gzip`. The zero data is clearly compressed by both `gzip` and SMACHE, since all blocks are common, although SMACHE imposes slightly more overhead. The random data is not compressed by either SMACHE or `gzip`, since there is very little self-similarity or compressability. We can see here that the overhead imposed by SMACHE itself is minimal – primarily it is from the database backend. This overhead is easily removable by using a more appropriate backend, we are not concerned with this aspect for this implementation.

SMACHE achieves expected good performance on the duplicated random data set. Discounting unnecessary database overhead, it handily beats the uncompressed version and `gzip`, since the data set demonstrates significant self-similarity. The amount of stored data is marginally more than half the original size of the random data, as expected. Note that this also demonstrates the benefits of a content-sensitive block algorithm, since a fixed-size block algo-



(a) Zeros (b) Random (c) Near-Duplicate Random

Figure 4. The performance of SMACHE on three simple synthetic data sets.

rithm would not see repeated blocks due to the small modification of the random data.

4.2 Biological Data

We evaluated the performance of SMACHE in storing biological data by caching several complete genomes. Each genome was several gigabytes in size. It is difficult to know exactly what kinds of biological data will be commonly used together by computational biologists, which is why SMACHE was designed as a general-purpose mechanism. We feel that storing related genomes is a reasonable proof-of-concept approach.

For all biological data, we use a block algorithm of Rabin-Harp rolling hashes with a mean blocksize of 512 bytes. Although using different blocksizes and parameters for this algorithm yields interesting results, we found 512 bytes to give reasonable performance and omit further analysis for the sake of brevity.

Single Genome

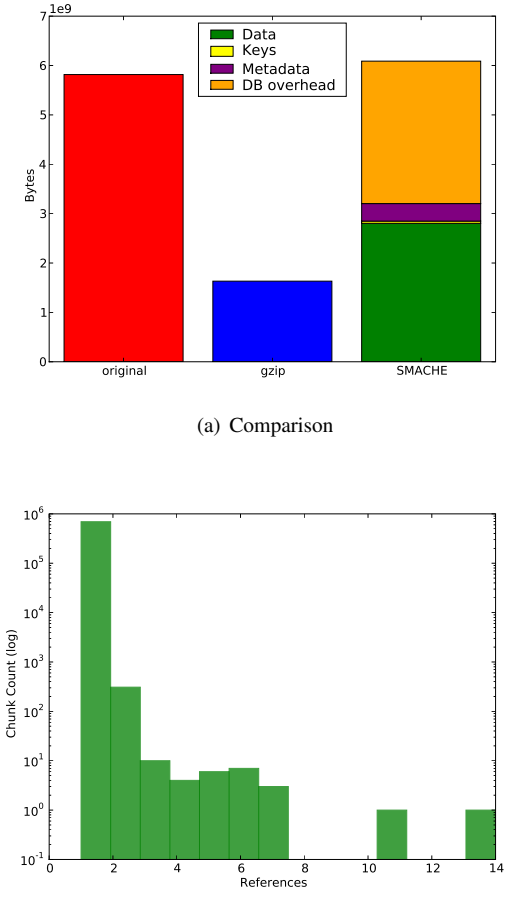
To evaluate the self-similarity of a basic biological data set, we created a cache consisting of the FASTA formatted files compromising the genome of the common mouse.

We see in Figure 5(a) that SMACHE achieves reasonable performance on the mouse genome. However, the vast majority of this performance is due to the level of compression achieved. As shown in Figure 5(b), approximately 90% of data blocks are compressed, and a overall compression ratio of just above 50% is achieved. Although the optimal compression ratio for biological data is 25% or below, the FASTA files do contain other information and the compression algorithms used are completely general-purpose.

Figure 5(c) shows that although there are several blocks that were are repeated over 60 times, the majority of blocks appear only once in the genome. For example, over one million blocks were unique, whereas approximately 10 thousand blocks were repeated twice. Figure 5(d) shows similarly that few sequences of blocks (metadata blocks) were repeated. This is expected, since relatively few blocks were repeated. Although we saw a single metadata block repeated eight times, we expect that this is equivalent to a zero page (perhaps missing genomic data or a long repeat in the genome).

Related Genomes

We combined the complete mouse genome and complete human genome into a single cache using `smachezip` in order to evaluate the performance of the system on related biological data. Since the mouse and humans are both advanced mammals, we expect to see significant sharing.

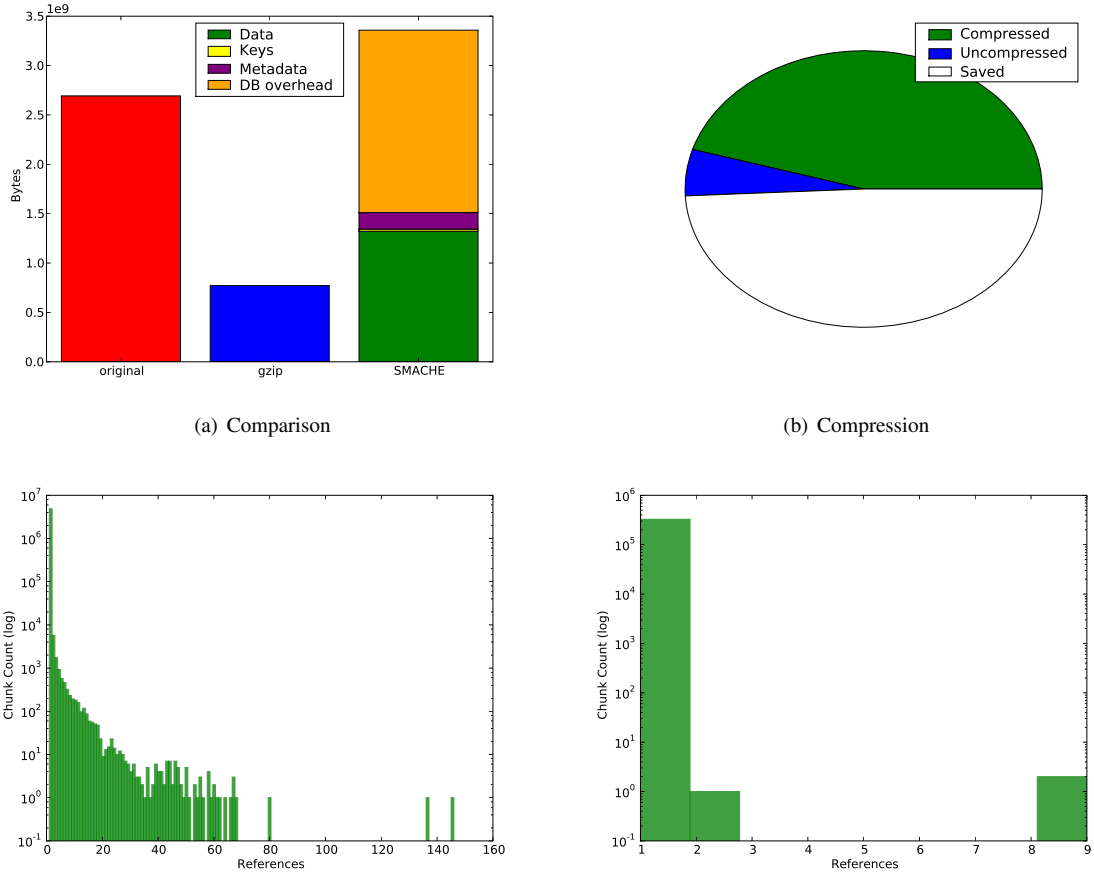


(a) Comparison

(b) Metadata Reference Count Histogram

Figure 6. Caching the complete mouse genome and complete human genome.

Figure 6(a) shows that the performance of SMACHE is similar to the case of a single genome. Relative performance to `gzip` was only marginally better. Most of the gains come from compression as opposed to sharing. We expect that this is due to a large number



(a) Comparison

(b) Compression

(c) Data Reference Count Histogram

(d) Metadata Reference Count Histogram

Figure 5. Caching the complete genome of the common mouse.

of tiny differences spread through the genomes that made exact block matches rarer than we would have liked.

Although, interestingly we did see some small amount of sharing between the genomes. For example, Figure 6(b) shows a histogram of the reference counts for the metadata blocks. The fact that these are significantly higher indicates one of two things: humans have a lot of internal genomic repetition of long sequences or there was sharing of a few long sequences between humans and mice. We feel it was likely a combination of the two.

Multiple Genomes

Finally, we tested performance of SMACHE when caching a larger set of genomes. Due to the size of the data, we limited ourselves to four animals: the common mouse, human, dog and chicken.

We found that the performance of SMACHE related to `gzip` was similar to the case of related genomes and omit graphs for that reason. Again, we expect that a very large number of tiny differences made exact block matches difficult. It may be worth exploring smaller block sizes, differencing algorithms and fuzzy block matches for genomic data. Unfortunately, a Rabin-Karp-based block algorithm with a mean size of 512 bytes did not produce the level of similarity that we expected.

4.3 Virtual Machine Images

For all VM image data, we use a fixed size block of 512 bytes. This is equivalent to the block size of the virtual disk and will allow us to capitalize on the frequency of zeroed blocks, among other things.

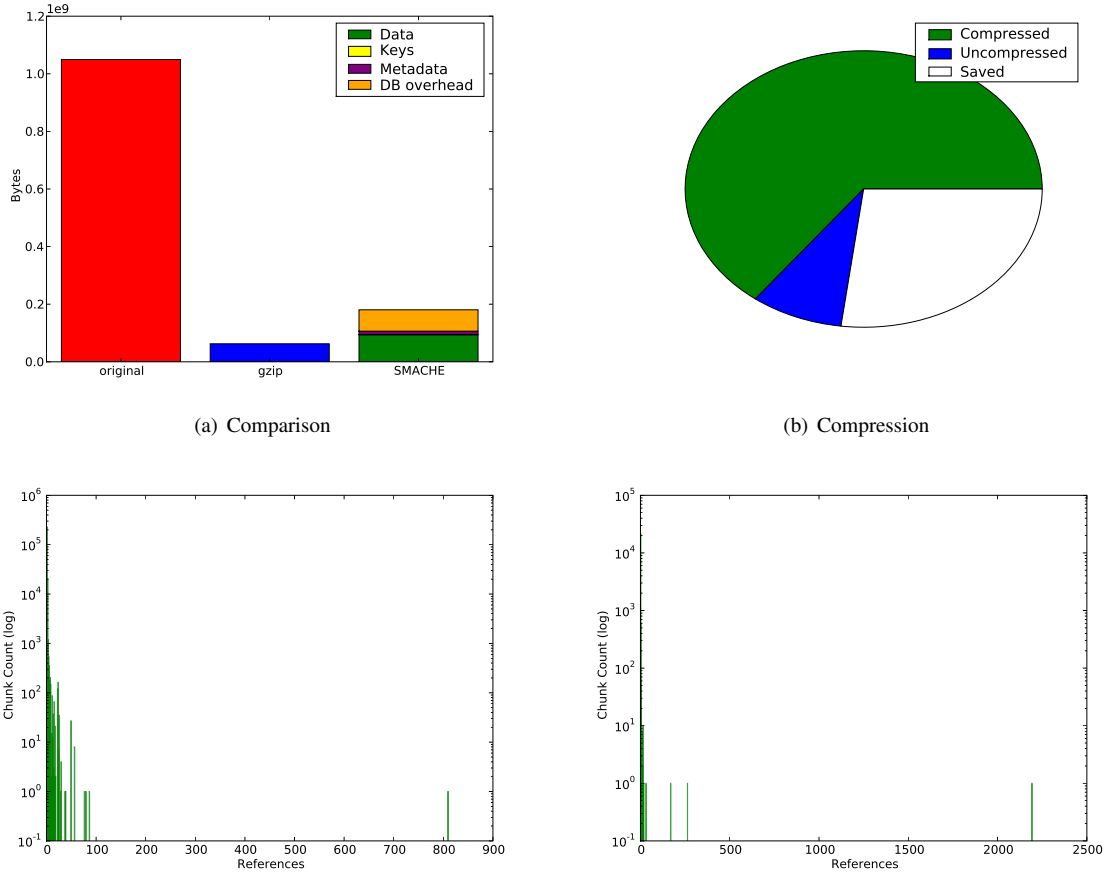
Single Virtual Machine Image

To establish a baseline, we downloaded a Debian VM image from `jailtime.org` and created a cache containing this image using the `smachezip` tool.

SMACHE stores a single VM image very efficiently, coming very close to `gzip` in terms of space efficiency. We find that it is only tens of megabytes above `gzip` when the unnecessary overhead associated with the database is discounted.

For non-redundant data stored, we achieve a compression ratio of about 75%. This poor ratio is unsurprising, as the data in a VM image is generally binary and SMACHE compression can operate on only small blocks. With this amount of data, there is rarely enough information to achieve reasonable compression with fairly uniformly distributed binary data. Figure 7(b) shows the percentage of blocks that were compressed.

Figure 7(c) shows a surprising number of blocks that have 10, 20 and even 50 references. These are likely patterns such as compiler-inserted stubs (e.g., as crt0.o), shared library hooks and trampolines, template code, and filesystem structures such as blank



(a) Comparison

(b) Compression

(c) Data Reference Count Histogram

(d) Metadata Reference Count Histogram

Figure 7. Caching a single Debian Virtual Machine image.

inodes. The majority of the savings, however, were likely due to a few highly repeated blocks (such as a zero block). We see a single block with a reference count of over 800.

Figure 7(d) shows that longer sequences are rarely repeated. This is sensible, since the layout of the filesystem will largely be block-based, and not as a complete sequence as in the biological example.

Related Virtual Machine Images

We explore the effectiveness of SMACHE storing related VM images by creating a cache with two VM images: the unmodified image from the case above, and the same image after an upgrade and mild usage. To derive the modified image, the unmodified Debian image was first copied and upgraded through the standard `apt-get upgrade` procedure. The upgrade affected several hundred packages (the majority of the software found on the image). Then, the modified image was used for development of SMACHE over the course of several hours, additionally requiring that several extra packages be installed.

Figure 8 shows the performance of SMACHE compared to a flat cache and `gzip`. Surprisingly, once overhead from the database is discounted, SMACHE stores data **more efficiently** than even `gzip`, while still giving random access semantics. We see this because a large number of blocks are shared across the two images, since the percentage of blocks with references greater than one is

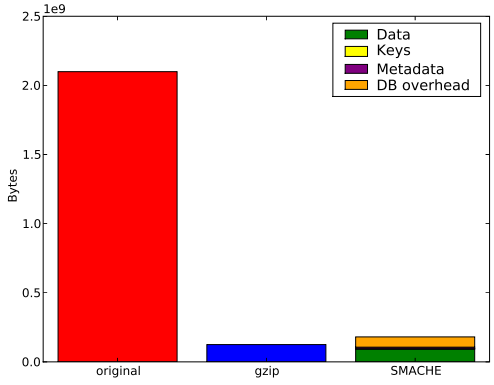


Figure 8. Caching two related Virtual Machine images.

significantly higher than in the case of a single VM image; the histogram is not shown here since visibly this is not obvious. This is a remarkably result, since non-trivial changes were introduced to the second VM image. Most of the savings are from sharing

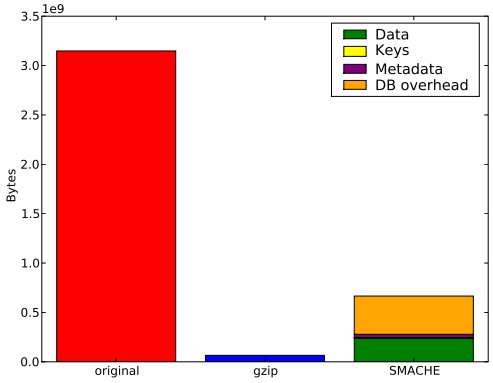


Figure 9. Caching two unrelated Virtual Machine images.

between the images; compression helps only marginally, as in the case of a single VM image.

We can conclude that SMACHE would be very effective at storing a large number of related VM images. In compute clouds this is likely to be a very common scenario; an approach such as SMACHE appears very promising.

Different Distributions

We additionally tested the efficiency of SMACHE in storing completely unrelated VM images. In addition to the basic Debian VM image described above, we cached a Fedora Core 9 image also downloaded from `jailtime.org`.

Figure 9 shows less impressive performance than caching related VM images. For the most part, we see that the space taken is the sum of storing two independent images. However, this is not unreasonable as these images contain completely different software packages with completely different versions. All configuration files and metadata within the image are also different. We find that sharing between VM images is not as significant in this case of related VM images, since relatively fewer blocks have more than one reference count.

As in the case of a single image, we see significant savings realized through a couple of highly repeated blocks at approximately 2600 and 3000 references each. Compression also helps here, achieving a ratio of approximately 50%.

We can conclude that although SMACHE does not see significant savings for unrelated images, there is little disadvantage here. We still realize savings through internal self-similarity and compression of individual blocks.

5. Conclusion

Cloud and cluster computing is an important factor in tackling "big data" problems. Systems support for distributed programming paradigms such as Map-Reduce and SnowFlock are still young. SMACHE implements a general-purpose space-efficient cache which services can use to store both biological or scientific data as well as program data. This cache represents an important building block for scalable storage systems in cluster computing.

In particular, we saw very promising results for storing related VM images, actually beating standard compression techniques while still providing random access semantics. Results storing biological data sets were not as stunning, however we feel that there is room for improvement by exploring better block algorithms, performing near blocks matches and storing differential data. In any case, SMACHE handily beat out the flat caching mechanism, likely making it an more appropriate choice than either no compression or standard compression techniques in most scenarios.

References

[1] The drive for the 1000 dollar genome. http://www.bio-itworld.com/issues/2007/may/cover-story/.

[2] Filesystem in userspace. http://fuse.sourceforge.net.

[3] memcached. http://www.danga.com/memcached.

[4] M. Duc Cao, T. I. Dix, L. Allison, and C. Mears. A simple statistical algorithm for biological sequence compression. In *DCC '07: Proceedings of the 2007 Data Compression Conference*, pages 43–52, Washington, DC, USA, 2007. IEEE Computer Society.

[5] D. Gupta, S. Lee, M. Vrable, S. Savage, A. C. Snoeren, G. Varghese, G. M. Voelker, and A. Vahdat. Difference engine: Harnessing memory redundancy in virtual machines. In *8th USENIX Symposium on Operating System Design and Implementation (OSDI 2008)*. USENIX, December 2008.

[6] R. M. Karp and M. O. Rabin. Efficient randomized pattern-matching algorithms. *IBM J. Res. Dev.*, 31(2):249–260, 1987.

[7] H. A. Lagar-Cavilla, J. Whitney, A. Scannell, P. Patchin, S. M. Rumble, E. de Lara, M. Brudno, and M. Satyanarayanan. Snowflock: Rapid virtual machine cloning for cloud computing. In *Third European Conference on Computer Systems (Eurosys 2009)*, Nuremberg, Germany, April 2009.

[8] T. Matsumoto and K. S. H. Imai. Biological sequence compression algorithms. *Genome Informatics*, 11:43–52, 2000.

[9] M. A. Olson, K. Bostic, and M. Seltzer. Berkeley db. In *ATEC '99: Proceedings of the annual conference on USENIX Annual Technical Conference*, pages 43–43, Berkeley, CA, USA, 1999. USENIX Association.

[10] T. Suel, P. Noel, and D. Trendafilov. Improved file synchronization techniques for maintaining large replicated collections over slow networks. In *In Proc. of the Int. Conf. on Data Engineering*, pages 153–164, 2004.

[11] D. Teodosiu, N. Bjorner, Y. Gurevich, M. Manasse, and J. Porkka. Optimizing file replication over limited bandwidth networks using remote differential compression. Technical report, Microsoft Corporation, 2006.

[12] A. Tridgell and P. Mackeras. The rsync algorithm. Technical report, Australian National University, 1998.