Parallel Accelerated Custom Correlation Coefficient Calculations for Genomics Applications

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Abstract

The massive quantities of genomic data being made available through gene sequencing techniques are enabling breakthroughs in genomic science in many areas such as medical advances in the diagnosis and treatment of diseases. Analyzing this data, however, is a computational challenge insofar as the computational costs of the relevant algorithms can grow with quadratic, cubic or higher complexity—leading to the need for leadership scale computing. In this paper we describe a new approach to calculations of the Custom Correlation Coefficient (CCC) between Single Nucleotide Polymorphisms (SNPs) across a population, suitable for parallel systems equipped with graphics processing units (GPUs) or Intel Xeon Phi processors. We describe the mapping of the algorithms to accelerated processors, techniques used for eliminating redundant calculations due to symmetries, and strategies for efficient mapping of the calculations to many-node parallel systems. Results are presented demonstrating high per-node performance and near-ideal parallel scalability with rates of more than four quadrillion ($4 \times 10^{15}$) elementwise comparisons achieved per second on the ORNL Titan system. In a companion paper we describe corresponding techniques applied to calculations of the Proportional Similarity metric for comparative genomics applications.

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1. Introduction

Computation of the mathematical relationships between pairs of vectors is required in many science domains. In the field of genomics, the Custom Correlation Coefficient (CCC) \cite{1} was developed to calculate the correlation between mutations, or Single Nucleotide Polymorphisms (SNPs), across a population of individuals. This can be used to identify groups of SNP alleles which tend to co-occur in a population, and consequently can be used to find combinations of SNP alleles which associate with certain phenotypes, such as a disease phenotype \cite{2}. CCC also takes into account genetic heterogeneity and finds correlations...
between SNP alleles which co-occur in portions of the population, not requiring co-occurrence across the whole population.

The effectiveness of CCC has been demonstrated in diverse domains. It has been used to identify genetic patterns exhibiting highly significant associations with both hypertensive heart disease [1] and psoriasis [2]. In another study, CCC was utilized to reveal genetic coadaptation between vitamin D receptor and skin color genes, suggesting parallel selective responses to environmental transitions as humans ventured out of Africa [3]. Interestingly, the CCC analysis of HapMap [4] data revealed a large-scale genetic pattern on human chromosome 14 [5]. This discovery suggests that two completely divergent evolutionary paths rapidly progressed in our past, presumably achieving the shared goal of enhancing gephyrin, a gene that is vital for signal transmissions in the human brain. Note that the HapMap data are arguably the most extensively studied SNP data available, yet this pattern was not previously identified by others – demonstrating CCC’s ability to identify combinatorial patterns of correlated SNP alleles within genome-wide data that are missed by other methods.

The explosive growth in genomic data has opened unprecedented levels of opportunity for addressing fundamental questions of importance in genomic sciences. However, the requisite computational methods are expensive, insofar as the computational complexity of general pairwise vector comparison methods is quadratic in the number of vectors, and the complexity is even higher for methods comparing three or more vectors at a time as is required in some cases. To perform large scale studies, it has thus become necessary to use high performance leadership computing systems possessing thousands of compute nodes equipped with advanced hardware such as accelerated manycore processors.

In this paper we describe new approaches to performing CCC calculations on leadership class systems equipped with GPUs. We describe implementations of CCC methods which attain high absolute performance on GPUs, use asynchronous methods to overlap operations, avoid the performance penalty of performing redundant and unnecessary computations, and exhibit near-ideal scaling to thousands of compute nodes.

Substantial recent work has focused on the problem of comparing pairs, triples or larger subsets of a set of vectors efficiently by means of advanced computational methods such as the use of parallelism, accelerated GPU or Intel Xeon Phi processing, or both. A broad overview of epistasis detection in comparative genomics including computational issues pertaining to parallelism and GPU acceleration is given in [6]. The GBOOST code, discussed in [7], is a gene-gene interaction code for 2-way studies optimized for single GPUs using encoding of gene data into bit strings with avoidance of redundant computations; [8] describes GWISFI, a single-GPU code for 2-way GWAS calculations. [9] develops a UPC++ code for gene-gene interaction studies for small numbers of GPUs and Intel Phi processors exploiting vector hardware and hardware population count instructions. [10] considers 3-way interactions on a node with 4 GPUs. [11] develops parallel tensor computation methods, structurally similar to 3-way metrics computations, with particular attention to avoiding redundant computations; however, the work does not consider GPUs or shaping of the computational regions to accommodate processors with long vector lengths. [12] discusses similarity metric calculations for chemical informatics applications on single GPUs using space filling curve methods and hardware population count instructions; it recognizes the correspondence of these calculations to BLAS-3 matrix-matrix product computations and pays close attention to optimizing memory accesses. [13] considers 2-way studies on compute clouds using MapReduce on conventional CPUs. [14] adapts existing packages to perform 2-way CPU and GPU studies and 3-way CPU studies on as many as 200 cores in parallel. [15] performs k-way GWAS studies for arbitrary k with consideration of load balancing and elimination of redundancies on a 4096-node IBM Blue Gene/Q system; results for a single GPU are also presented. [16] performs 2-way analyses on up to 126 nodes of the Intel Phi-based Stampede system (cf. [17]). [18] considers 2-way computations on thousands of compute cores with good scalability and good absolute performance on conventional CPUs. Finally, recent work in [19] considers k-selection similarity search methods with applications to image data with results for small numbers of GPUs; that work however focuses primarily on the k-selection problem for nonexhaustive inexact similarity search, a different problem from what is considered here.

This work is to our knowledge the first successful effort to combine all the needed elements for performing large-scale 2-way and 3-way vector comparison studies on leadership-class systems, including: high performance usage of accelerated processors, effective use of deep memory hierarchies, avoidance of unneeded
2. The Custom Correlation Coefficient

2.1. The 2-way metric

We assume a set of \( n_v \) vectors of length \( n_f \) elements \( \{v_i\}_{i=1}^{n_v} \) with \( v_i \in \{S_2\}^{n_f} \) and \( v_i = \{v_{i,q}\} \). Here \( S_2 = S \times S = S^2 \) where \( S = \{0, 1\} \), thus each vector entry \( v_{i,q} \) is itself a vector with two entries \( (v_{i,q})_r \) taken from \( S \). In practice, the \( v_i \) are SNPs each of whose entries \( v_{i,q} \in S_2 \) represents a pair of alleles, with a possibly different allele interpretation for each column \( i \), and \( n_f \) is the number of samples.

For \( a, b \in S \) define the indicator function \( \chi_a \) by \( \chi_a(b) = 1 \) if \( a = b \), otherwise 0. Let \( \rho_{i,q}(a) = \sum_r \chi_a((v_{i,q})_r) \), the count of entries with the value \( a \) in \( v_{i,q} \). The frequency of allele \( a \) for SNP \( v_i \) is then

\[
f_i(a) = \frac{1}{2n_f} \sum_{q=1}^{n_f} \rho_{i,q}(a). \tag{1}
\]

Clearly \( f_i(0) + f_i(1) = 1 \). Also let \( \rho_{i,j,q}(a,b) = \rho_{i,q}(a) \cdot \rho_{j,q}(b) \) and

\[
f_{i,j}(a,b) = \frac{1}{4n_f} \sum_{q=1}^{n_f} \rho_{i,j,q}(a,b). \tag{2}
\]

Note \( \sum_{a,b \in S} f_{i,j}(a,b) = 1 \). Then the 2-way CCC comparison for \( a, b \in S \) assuming a fixed constant \( \gamma = 2/3 \) is

\[
CCC_{i,j}(a,b) = f_{i,j}(a,b)(1 - \gamma f_i(a))(1 - \gamma f_j(b)). \tag{3}
\]

The functions \( f_{i,j}(\cdot) \), and thus \( C_{i,j}(\cdot) \), are symmetric in \( i \) and \( j \). Thus to compute all unique values \( \{f_{i,j}(a,b)\}_{i,j,a,b} \) for distinct \( i \) and \( j \) requires \( 4n_fn_v(n_v - 1)/2 = O(n_v^2) \) operations. On the other hand, \( \{f_i(a)\}_{i,a} \) requires only \( 2n_fn_v = O(n_f n_v) \) operations. Due to its greater computational cost, the efficient calculation of \( \{f_{i,j}(a,b)\} \) will be the chief focus of this work.

An interpretation of the \( f_{i,j} \) component of the 2-way CCC calculation is shown in Figure 1. Here we let \( n_f = 1 \) and \( n_v = 2 \). For the first entry of \( v_1 \) and of \( v_2 \), each containing two binary entries as shown, all four pairings of the left two entries and the right two entries are selected and enumerated, with four resulting tuple values, each taken from a set of four possible combinations \( (0,0), (0,1), (1,0) \) and \( (1,1) \). These tuples are then tallied by value to count the frequency of each possible tuple. For the general case of \( n_f > 1 \), the additional entries are handled in the same way, with the counts of each pairing tally summed into the result table shown at the right.

2.2. The 3-way metric

The previous section described CCC for evaluating pairs of SNPs; next we expand this to the evaluation of SNP trios. The 3-way CCC comparison for \( a, b, c \in S \) and vectors \( v_i, v_j, v_k \) and a fixed constant \( \gamma \) is defined by

\[
CCC_{i,j,k}(a,b,c) = f_{i,j,k}(a,b,c)(1 - \gamma f_i(a))(1 - \gamma f_j(b))(1 - \gamma f_k(c)). \tag{4}
\]
Here,

\[ f_{i,j,k}(a, b, c) = \frac{1}{8n_f} \sum_{q=1}^{n_f} \rho_{i,j,k,q}(a, b, c) \]  

(5)

for \( \rho_{i,j,k,q}(a, b, c) = \rho_{i,q}(a) \cdot \rho_{j,q}(b) \cdot \rho_{k,q}(c) \).

Due to symmetries in \( i, j \) and \( k \), only \( 8n_v(n_v - 1)(n_v - 2)/6 \) unique values of \( \{f_{i,j,k}(a, b, c)\}_{i,j,k,a,b,c} \) need be computed for distinct \( i, j \) and \( k \), requiring \( 8n_f n_v(n_v - 1)(n_v - 2)/6 = O(n_f n_v^3) \) operations. The dominance of this computational expense over the calculation of the \( f_i(a) \) values makes this the primary focus of attention.

Figure 2 gives an interpretation, for \( n_f = 1 \) and \( n_v = 3 \). Here \( n_f = 1 \) and \( n_v = 3 \) so that, again, each vector has one entry which is itself a 2-vector of binary entries. All eight combinations of vector entries are sampled, and the counts of these triples are tallied into a table whose entries correspond to the eight possible combinations of three binary values.

3. Mapping to manycore processors

3.1. The 2-way metric

Let us define \( B = V^T \circ_2 V \) to satisfy \( (B_{i,j})_{a,b} = f_{i,j}(a, b) \). It can be observed that the basic structure of the computation of the \( f_{i,j}(a, b) \) values—namely, the summing of values derived from corresponding entries
Table 1: Values of $X_{j,ξ}$

| $v_j$ | $V$ | $X_{j,1}$ | $X_{j,2}$ | $X_{j,3}$ |
|-------|-----|-----------|-----------|-----------|
| 0,0   | 0,0 | 0,0       | 1,0       | 1,0       |
| 0,0   | 0,1 | 0,1       | 1,0       | 1,0       |
| 0,0   | 1,1 | 1,1       | 1,0       | 1,0       |
| 0,1   | 0,0 | 1,0       | 0,0       | 1,0       |
| 0,1   | 0,1 | 1,0       | 0,1       | 1,0       |
| 0,1   | 1,1 | 1,0       | 1,1       | 1,0       |
| 1,1   | 0,0 | 1,0       | 1,0       | 0,0       |
| 1,1   | 0,1 | 1,0       | 1,0       | 0,1       |
| 1,1   | 1,1 | 1,0       | 1,0       | 1,1       |

of each pair of vectors—is identical to the structure of the general matrix-matrix product computation (GEMM), with the pairwise multiplication of scalar vector elements in the GEMM replaced with a tally into a 2X2 table. To solve this efficiently on manycore compute nodes, we follow the approach of [20], adapting the GEMM kernel from an optimized dense linear algebra library, in this case MAGMA[21] targeting GPUs, to accelerate this operation.

In [20] we implemented the Proportional Similarity metric by replacing the scalar multiplication operation of the GEMM with the minimum operation on two scalar values. Here however we have a tally operation which requires special considerations to implement efficiently. For CCC, since every entry of $v_i$ is composed of only two bits, significant savings in computation time as well as storage is possible by packing the bits of many vector entries into a single compute word. We use the MAGMA double complex ZGEMM operation, for which each MAGMA vector entry is composed of two 64-bit words, so that a single ZGEMM vector entry can hold 64 $v_i$ entries. For fixed $i$ and $j$, four $f_{i,j}(a,b)$ (integer) values must then be accumulated. To fit this into a result value of two 64-bit doubles for the ZGEMM, we assign 25 bits of the mantissa of each of the two floating point numbers to store each result. This allows $n_f$ to be as large as $2^{23} - 1 = 8,388,607$, without loss of precision from overflow of the mantissa or mixing of the two integer components stored in each word. This limit is far above the typical requirements for the targeted calculations. The resulting modified ZGEMM operation we refer to here as mGEMM2.

For each pair of corresponding double complex vector entries for which a tally is performed, it is efficient to use bitwise operations. In the implementation, for each tally target $(0,0)$, $(0,1)$, $(1,0)$ and $(1,1)$, corresponding words are appropriately shifted, masked and XORed to obtain a word for which each bit is set to 1 if the original pair of bits corresponds to the respective tally table entry and 0 otherwise. Then the CUDA intrinsic \texttt{popcll()} corresponding to a hardware population count operation is used to sum the number of bits of the word set to 1 and accumulate the result. The population count operation is supported in hardware for some conventional x86 CPUs as well; if not, it can typically be implemented with small numbers of machine instructions; see for example [22], [23]. In the implementation, care must be taken for the case when $n_f$ is not a multiple of 64 so that the tallies corresponding to the zero padding are corrected for.

Though we do not pursue the topic here, it is likely that libraries optimized to other processor architectures, such as PLASMA [24], BLIS [25] and OpenBLAS [26] would provide similar opportunities for improving performance for conventional processors and Intel Phi.

3.2. The 3-way metric

The 3-way method cannot be mapped directly to a modified GEMM framework using the same approach, insofar as in this case the tally table entries would need to be reduced to 12 bits to fit into two double precision words of the ZGEMM, limiting $n_f$ to size 4095 or less, inadequate for many problems. Thus an alternative approach is needed.
To solve this problem, the basic approach taken here is a two-step process. First, for given $V$ and a fixed $v_j$ we construct modified matrices $X_{j,\xi}$, $1 \leq \xi \leq 3$, each of the same dimension as $V$. Second, we calculate $B_{\xi} = X_{j,\xi}^T \circ_3 V$ for an operator $\circ_3$ representing a modified 2-way calculation from which it is possible to reconstruct the 3-way tally values for $v_i$, $v_j$ and $v_k$ for $1 \leq i, k \leq n_v$.

For the first step, the entry $(X_{j,\xi})_{q,p}$ is formed from the entries $v_{j,q}$ and $(V)_{q,p}$ according to the rules shown in Table 1. The table gives values for the $n_f = 1$ case; for the general case, corresponding rows of $v_j$ and $V$ are handled likewise. Here, for convenience the entries of $v_j$ and $V$ that have the value $(1,0)$ are omitted since they have an identical result on the calculation as $(0,1)$ insofar as the CCC result tally values do not differentiate between these cases.

The aim here is to let $X_{j,1}$, $X_{j,2}$ and $X_{j,3}$ each be the corresponding value of $V$ (with $(1,0)$ mapped to $(0,1)$) if $v_j$ equals $(0,0)$, $(0,1)$ and $(1,1)$ respectively and the “null” indicator value of $(1,0)$ otherwise. We refer to this modified GEMM operation as mGEMM3.

After the entries $X_{j,\xi}$ are formed, the matrices $B_{j,\xi} = X_{j,\xi}^T \circ_3 V$ are calculated similarly to the previously described 2-way method based on modified GEMMs. Here the operator $\circ_3$ represents the same tally process as used for the 2-way method described above except that $X_{j,\xi}$ values equal to the null indicator $(1,0)$ are discarded and not used in the tally.

It is then straightforward to construct the 3-way tallies from the constituent 2-way tallies $\{B_{j,\xi}\}$ of $X_{j,\xi}$. The matrix $B_{j,1}$ contributes tallies for entries of $v_j$ equal to $(0,0)$, and similarly $B_{j,2}$ for $(0,1)$ and $B_{j,3}$ for $(1,1)$. For each $B_{j,\xi}$, $1 \leq \xi \leq 3$, the four 2-way tally results for each vector triple must be mapped to the appropriate eight table entries for the 3-way tally associated with this vector triple. The mapping is given by

$$
\begin{align*}
&f_{i,j,k}(0,0,0) = 2((B_{j,1})(i,k))(0,0) + ((B_{j,2})(i,k))(0,0), \\
&f_{i,j,k}(0,0,1) = 2((B_{j,1})(i,k))(0,1) + ((B_{j,2})(i,k))(0,1), \\
&f_{i,j,k}(0,1,0) = 2((B_{j,1})(i,k))(1,0) + ((B_{j,2})(i,k))(1,0), \\
&f_{i,j,k}(0,1,1) = 2((B_{j,1})(i,k))(1,1) + ((B_{j,2})(i,k))(1,1), \\
&f_{i,j,k}(1,0,0) = 2((B_{j,3})(i,k))(0,0) + ((B_{j,2})(i,k))(0,0), \\
&f_{i,j,k}(1,0,1) = 2((B_{j,3})(i,k))(0,1) + ((B_{j,2})(i,k))(0,1), \\
&f_{i,j,k}(1,1,0) = 2((B_{j,3})(i,k))(1,0) + ((B_{j,2})(i,k))(1,0), \\
&f_{i,j,k}(1,1,1) = 2((B_{j,3})(i,k))(1,1) + ((B_{j,2})(i,k))(1,1).
\end{align*}
$$

The 3-way calculation thus requires three modified GEMM operations, compared to one for the 2-way method. Insofar as each 3-way vector triple tally requires eight values compared to four for each 2-way pair, and the path length (Figure 2) is three for the 3-way method compared to two for the 2-way method (Figure 1), we believe it is near-optimal for the 3-way method to require roughly 3X the work of the 2-way method as is the case in this implementation.

4. Multi-node parallelism

The details of the parallel implementation are essentially identical to those for the Proportional Similarity metric as described in detail in [20]. Here we give the main ideas in summary form.

Parallelism is obtained by decomposing both the $n_f$ problem dimension and the $n_v$ problem dimension across $n_{pf}$ and $n_{pv}$ nodes respectively, resulting in $n_{pf} \times n_{pv}$ elements per node. A third axis, $n_{pr}$, is used to apply additional parallelism across the computation of the result values.

The $n_{pf}$ parallelism axis requires a parallel reduction operation. The $n_{pv}$ axis requires carefully scheduled point-to-point communications so that every vector can be compared against every other vector.

For the 2-way method, the result values form a 2-D square matrix of values with an imposed decomposition into smaller square blocks due to the $n_{pv}$ parallelism. To avoid computing redundant values resulting from symmetry of the matrix, results are computed only for a block circulant subset of the blocks. Each
The $n_{pv}$-parallelism compute node is responsible for computing a block row of this matrix. The $n_{pv}$ parallel axis is used to parallelize the computation of the blocks of this block row.

For the 3-way method, the result values make up a cube-shaped 3-D array of values, implicitly decomposed into smaller cubes by the $n_{pv}$ parallel decomposition. A scheme is implemented so that only a subset or “slice” of values is calculated for each block, this subset chosen to represent each of the unique values in the result exactly once. Each $n_{pv}$-parallelism compute node is responsible for computing a 2-D slab of the results cube. The $n_{pv}$ axis of parallelism is deployed so that the blocks in this slab can be computed in parallel.

The 3-way method allows an additional setting, $n_{st}$, which allows the metrics computation to be broken into multiple stages. To reduce the main memory storage costs for the metrics values, a run can be performed for which only a single stage of results is computed.

Asynchronous methods are used to overlap GPU computations, CPU computations, communications and transfers of data to and from the GPUs.

5. Implementation

The algorithms described here are implemented in the CoMeT parallel genomics code. This code is written in C++, compiles with the GNU compiler suite and depends on MPI, CUDA and the modified versions of the MAGMA library. GNU Make and CMake are used for build management, and googletest is used for unit testing. The clang-format source code tool from the clang compiler package is used for source code formatting, and Git is used for repository management.

OpenMP CPU threading is used to accelerate the parts of the computation that are not ported to the GPU by mapping execution to multiple CPU cores on the node; when possible, the CPU work is also hidden under the asynchronously launched GPU kernels to improve performance.

For making comparisons, each method has a reference (CPU-only) version, a (possibly optimized) CPU version, and a GPU version. A set of synthetic reference test cases is implemented for testing, designed to give the exact same bit-for-bit result for all code versions and for all parallel decompositions. Two types of synthetic problem are implemented: a version for which each vector entry is set to a randomized value, and a second version with randomized placement of entries specifically chosen so that the correctness of every result value can be verified analytically. A checksum feature using extended precision integer arithmetic computes a bit-for-bit exact checksum of computed results to check for errors when using synthetic inputs.

The code can be compiled under single or double precision. The precision setting for the CCC case affects only the accuracy of the calculation of the $f_i()$ values for the denominators; for the numerator computations, as described earlier the relevant computations are performed with double complex data types.

To modify MAGMA as needed for the algorithms, it is necessary to modify the two files in the MAGMA package `magmablas/gemm_stencil.cuh` and `magmablas/gemm_stencil_defs.h`. In particular, the macro definition for “fma” defining the fused multiply accumulate must be changed to make use of the appropriate tally operation.

6. Computational results

6.1. Overview

Experiments are performed on the ORNL Titan Cray XK7 system. Titan is composed of 18,688 compute nodes each equipped with an AMD Interlagos 16 core CPU and an NVIDIA Kepler K20X GPU connected via a PCIe-2 bus. The K20X GPU has peak single/double precision flop rate of 3,935/1,311 GF and peak memory bandwidth of 250 GB/sec. Each node contains 32 GB main memory and 6 GB GPU memory.

The software versions used are Cray OS version 5.2.82, Cray Programming Environment 2.5.5, GCC 4.9.3, MAGMA 1.6.2 and CUDA toolkit 7.5.18-1.0502.10743.2.1. For large node counts, it is in some cases necessary to set the environment variable `APRUN_BALANCED_INJECTION` to values such as 63 or 33 to avoid throttling of the communication network resulting from the algorithms’ communication patterns and causing performance loss.
Table 2: Kernel performance for single GPU case

|                | time (sec) | time per element pair |
|----------------|------------|-----------------------|
| mGEMM2         | 163.901    | 3.975e-12             |
| mGEMM3         | 217.294    | 5.270e-12             |
| ZGEMM, MAGMA   | 6.998      | 10.863e-12            |
| ZGEMM, cuBLAS  | 4.493      | 6.974e-12             |
| ZGEMM, theoretical peak | 3.931 | 6.102e-12 |

The primary use of the code is to solve very large problems not previously solvable; thus weak scaling behavior, for which the work per node is kept roughly constant as compute node count is increased, is the primary focus.

GPU-enabled runs are executed with one MPI rank and one GPU per Titan node. Reported execution times do not include I/O. The source code execution path for the algorithm is identical independent of the actual values contained in the input vectors; thus we expect performance for the synthetic datasets used here to be essentially identical to performance with actual genomics data.

6.2. Single GPU kernel performance

We first evaluate the raw performance of the modified GEMM kernels in comparison with the standard GEMM. We test the mGEMM2 and mGEMM3 operations described above, used for the 2-way and 3-way methods respectively. We use $n_v = 10,240$ vectors of length $n_f = 393,216$ 2-bit values corresponding to 6,144 double complex values. Timings are compared against the standard ZGEMM for matrices of the same size. Kernel times are taken from the CUDA Profiler and include kernel time only, without transfer or CPU times.

Results are shown in Table 2. Raw timings are shown as well as normalized times representing the time per pair of elements operated on, where an element is interpreted to be a double complex value except for the modified GEMM cases in which case it is a 2-bit value. The cost of mGEMM3 is higher than that of mGEMM2 due to additional masking operations needed. The modified GEMMs have 64X higher density of vector elements per double complex value, thus suggesting a higher throughput rate than ZGEMM is possible; however, instead of four FMAs per pair, a significant number of bitwise operations such as shifts, masks, logical operations and populations counts are required per element pair. Thus the modified GEMM normalized rates exceed the ZGEMM theoretical peak by a smaller value than expected. A side effect is that computational intensity is extremely high, suggesting potentially high processor utilization and favorable opportunities to hide communications and GPU data transfers under computations. The MAGMA ZGEMM rates are somewhat less than those of cuBLAS since the former is more targeted toward smaller cases required by other MAGMA operations. Further optimizations of the bitwise operations of the modified GEMMs will be a topic of further study.

6.3. Performance model

It is desirable to model algorithm performance in order to evaluate expected performance and also to give guidance regarding selection of tuning parameters. We assume here that mGEMM2 and mGEMM3 sizes are large enough to hide communications, GPU data transfers and CPU computations.

For the 2-way case, we define $\ell$, the “load,” to denote the number of blocks assigned to each node. Then the execution time of the algorithm is estimated by

$$\text{t} = t_C + t_{T,V} + \ell \cdot t_{G,2} + t_{T,M} + t_{CPU},$$

where $t_C$ is the time for communicating $n_fnvp$ vector elements per node for a parallel step, $t_{T,V}$ the time to transfer $n_fnvp$ vector elements to the GPU for a step, $t_{T,M}$ the time to transfer $nvp^2$ metrics values from
the GPU per step, \(t_{CPU}\) the time for denominator and quotient calculations per step and \(t_{G,2}\) the time for an mGEMM2 computation. The non-mGEMM2 times are included here to account for asynchronous pipeline startup and drain. It is evident that maximizing \(\ell\) (by limiting \(n_{pr}\)) makes it possible to approach peak mGEMM2 performance. mGEMM2 rates are determined empirically; the goal is to make the matrix dimensions \(n_{fp}\) and \(n_{vp}\) for the mGEMM2 computation as large as possible to maximize mGEMM2 efficiency. This suggests for a given problem it is desirable to reduce \(n_{pv}\) and \(n_{pf}\) until CPU or GPU memory is filled.

For the 3-way case, we again define the load \(\ell\), here representing the number of block slices computed by a node. Each slice is computed by a GPU pipeline of \(3(n_{vp}/6)/n_{st}\) mGEMM3 steps corresponding to the required three mGEMM3 operations to form each 3-way result. The execution time of the algorithm is estimated by

\[
t = t_C + t_{T,V} + \ell \cdot [3((n_{vp}/6)/n_{st})t_{G,3} + t_{T,V} + t_{T,M} + t_{CPU}].
\]

mGEMM3 performance is approached by increasing \(\ell\), and \(n_{vp}\) and decreasing \(n_{st}\), subject to memory constraints. Similarly to the 2-way case, \(n_{fp}\) and \(n_{vp}\) should be maximized in order to maximize mGEMM3 performance.

### 6.4. 2-way results

For 2-way weak scaling results we set \(n_f = 20,000\) elements per vector and \(n_{vp} = n_v/n_{pv} = 4,096\) vectors per node. We set the load \(\ell = 25\) and set \(n_{pr} = \lceil \lceil n_{pv}/2 + 1 \rceil /\ell \rceil \) and \(n_{pf} = 1\). The 2-way test runs are executed on up to 17,955 of Titan’s 18,688 compute nodes, or 96.1% of the system.

Results are shown in Figure 3. The left graph shows good weak scaling timing performance up to the full system. The method benefits from the very high computational intensity of the mGEMM2 kernel, dominating communication costs which it asynchronously overlaps. The right graph shows good weak scaling performance for the comparison rate per node. The maximum rate per node is \(232e9\) comparisons per node per second. Here a comparison defined as the operation between corresponding vector elements that produces four tally values to be accumulated. This rate compares well with the value of \(251.572e9\) comparisons per second per GPU derived from the 3.975e12 seconds per comparison per GPU indicated in Table 2.

![Figure 3: CCC 2-way weak scaling](image)

The method attains up to \(4.16e15\) comparisons (4.16 petacomparisons) of two vector elements per second. See Table 3.

### 6.5. 3-way results

The 3-way test runs are executed on up to 18,424 of Titan’s 18,688 compute nodes, or 98.6% of the system. We use \(n_f = 20,000\) elements per vector and \(n_{vp} = n_v/n_{pv} = 2,880\) vectors per node. We set the load \(\ell = 6\), \(n_{pr} = \lceil \lceil (n_{pv} + 1)(n_{pv} + 2)/\ell \rceil \rceil\), and \(n_{pf} = 1\) and compute the final stage of \(n_{st} = 16\) stages.

Weak scaling results are shown in Figure 4. The left graph shows near ideal weak scaling timing behavior for large problem sizes. The right graph shows the average number of vector element comparisons performed per node. Here one comparison is defined as a single 3-way calculation involving three vector elements that produces eight tallied results. Some inefficiencies exist a lower node counts due to load balancing effects in
Table 3: Maximum performance, CCC

| method   | comparisons per second |
|----------|------------------------|
| 2-way CCC | $4.16 \times 10^{19}$  |
| 3-way CCC | $1.01 \times 10^{15}$  |

the implementation; for larger node counts of interest, the impacts of this are minor. The rate approaches the peak achievable under the current scheme at large node counts. In particular, note that the 2-way comparison rate shown previously in Table 2 corresponds to $189.748 \times 10^9$ seconds per 2-way comparison; since a 3-way comparison requires three modified 2-way comparisons, we would expect each node to attain roughly $63 \times 10^9$ 3-way comparisons per second. The highest attained rate from Figure 4 shows $55 \times 10^9$ 3-way comparisons per second attained, a figure approaching the expected achievable figure.

![Figure 4: CCC 3-way weak scaling](image)

Table 3 shows the maximum operation and comparison rates attained at the highest node counts, up to $1.01$ 3-way petacomparisons per second.

7. Conclusions

We have defined a new set of algorithm implementations for performing 2-way and 3-way Custom Correlation Coefficient calculations for comparative genomics applications. Performance of up to four quadrillion vector element comparisons per second is demonstrated. To our knowledge this is the first simulation of its kind ever performed at this scale, demonstrating the capability to perform simulations that were until recently considered far beyond what is possible, enabling new kinds of science in comparative genomics.

Future work will include investigation of additional code performance improvements—for example, improved mGEMM2/mGEMM3 performance and lessening of overheads by additional code tuning. We anticipate the methods described here will be directly portable to alternative processor architectures such as Intel Xeon Phi. Due to the large amounts of data generated, use of these methods will also require careful engineering of computational science workflows in such a way that the entire workflow is well optimized for scientific discovery.

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