



Computing Hypergraph Homology in Chapel

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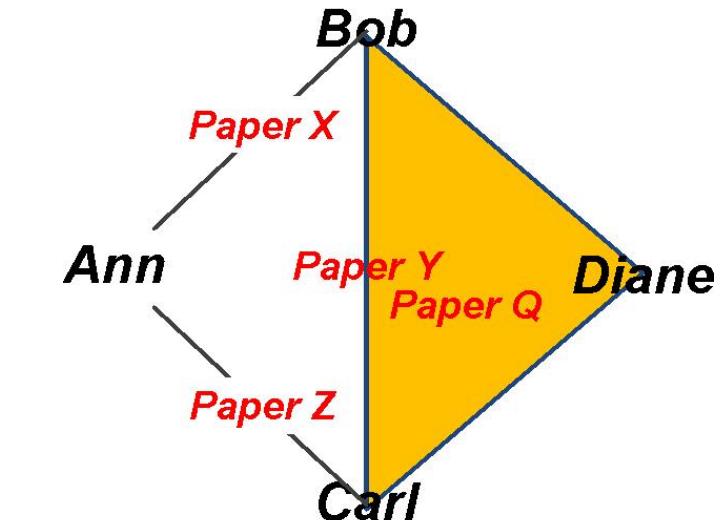
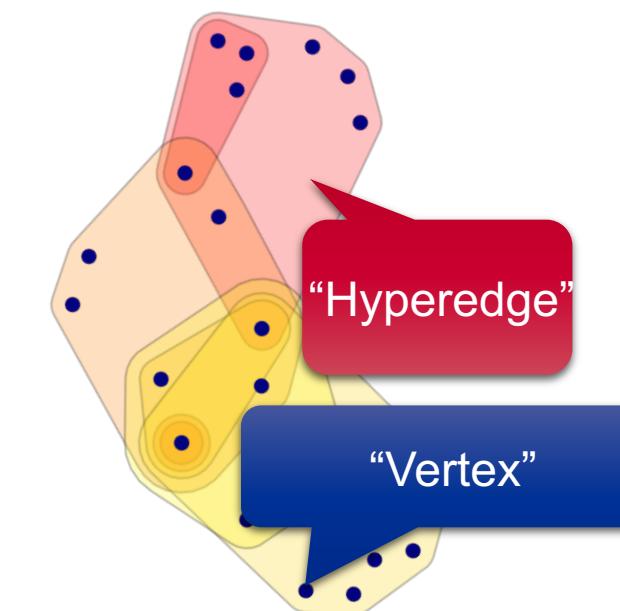
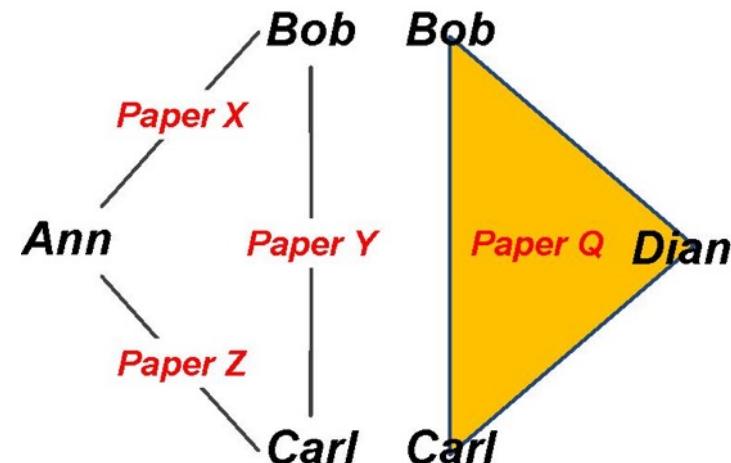


Outline

- Hypergraphs
- Hypergraph Homology Computation
 - Motivation
- Linear algebra operations: Chapel vs Python
- Hypergraph Homology Computation in Chapel
 - Two main steps
 - Optimizations
 - Experimental results

Hypergraphs

- **Graphs** model distributed interactions among entities
 - Questions of connectivity, reachability, density, clustering
- ***But multi-way interactions cannot be modeled natively by graphs!***
 - Requires higher coding strategies: Property graphs, reification, bipartite structures
- **Multi-Dimensional Graph: Hypergraph**



Hypergraph Homology Computation in Chapel

- Motivation:
 - Learn about missing data and their surrounding datasets.
 - Datasets and ASCs can be huge.
 - Leverage Chapel's parallel and distributed execution capability to run at scale.
- Two main steps:
 - Computing the boundary matrices
 - Computing the Smith Normal form of a matrix.
- Heavily involves matrix and linear algebra operations.

Homology Computation in Chapel (Cont.)

- Matrices are represented as 2D arrays in Chapel.
- Array-centric operations include:
 - Row and column interchange,
 - Pivot calculation,
 - Addition of rows and columns,
 - Rank computation,
 - Multiplication, and
 - Slicing
- In Chapel, such operations are very concise and more intuitive than in Python.
- While Chapel's linear algebra library performs various operations on matrices (such as singular value decomposition, LU decomposition etc.), our operations are in the Z_2 field, so we wrote our own.

Linear Algebra Operations: Chapel vs Python

Chapel

```

1 proc swap_rows(i,j,M) {
2     var N = M;
3     N[i, ..] <=> N[j, ..];
4     return N;
5 }
6 proc add_to_row(M,i,j,ri=1,rj=1) {
7     var N = M;
8     N[i, ..] = (ri * N[i, ..] + rj * N[j, ..]) % 2;
9     return N;
10 }
11 proc calculateRank(M) return + reduce
12     [i in M.domain.dim(2)] (max reduce M[.., i]);

```

Python (NumPy/sequential)

```

1 def rowswap(i,j,M):
2     N = copy.deepcopy(M)
3     N[i] = M[j]
4     N[j] = M[i]
5     return N
6 def add_to_row(M,i,j,ri=1,rj=1,mod=2):
7     N = copy.deepcopy(M)
8     N[i] = np.mod(ri*N[i] + rj*N[j],[mod])
9     return N
10 def calculaterank(M):
11     return np.sum(M)

```

Reduction intent: For each column, see if at least one 1, **in parallel**

Linear Algebra Operations: Chapel vs Python

Chapel

```
1 proc matmultmod (M, N, mod =2) {  
2     var C : [M.domain.dim(1), N.domain.dim(2)] int;  
3     forall (i,j) in C.domain {  
4         C[i,j] = (+ reduce (M[i, M.domain.dim(2)]  
5             * N[M.domain.dim(2), j])) % 2;  
6     return C;  
7 }
```

Python (NumPy/sequential)

```
1 def modmult(M,N,mod=2):  
2     return np.mod(np.matmul(M,N),mod)
```

Parallel matrix multiplication



Homology Computation in Chapel

Step 1. Boundary Matrix Computation: What We Will Do

- For example: Given a hypergraph with one hyperedge with four vertices:

$$_1 [\{ 0 \ 1 \ 2 \ 3 \}]$$

- Generate the ASCs (powerset of the hyperedge) and accumulate the k-cells in the corresponding bins:

$_1 \ 2 \rightarrow [\{ 0 \ 1 \ 2 \}, \{ 0 \ 1 \ 3 \}, \{ 0 \ 2 \ 3 \}, \{ 1 \ 2 \ 3 \}]$
$_2 \ 1 \rightarrow [\{ 0 \ 1 \}, \{ 0 \ 2 \}, \{ 0 \ 3 \}, \{ 1 \ 2 \}, \{ 1 \ 3 \}, \{ 2 \ 3 \}]$
$_3 \ 0 \rightarrow [\{ 0 \}, \{ 1 \}, \{ 2 \}, \{ 3 \}]$
$_4 \ 3 \rightarrow [\{ 0 \ 1 \ 2 \ 3 \}]$

0-cells

- Compute the boundary maps:

		1-cells														
		0-cells			1-cells			2-cells			3-cells			4-cells		
		1	2	3	1	2	3	1	2	3	1	2	3	1	2	3
		1	1	1	1	0	0	0	1	1	0	0	0	1	1	1
		2	1	0	0	1	1	0	0	1	1	0	0	1	1	1
		3	0	1	0	1	0	1	0	1	0	1	0	1	1	1
		4	0	0	1	0	1	1	1	0	1	1	1	0	0	1

Boundary Matrix Computation

Step 1a: Computing Abstract Simplicial Cell Complexes (ASCs)

Maintain one set per task per locale for gathering the ASCs

```
1 var cellSets : [0..#numLocales, 0..#here.maxTaskPar] → set(Cell);
```

Each edge computes the ASCs in parallel

```
1 var taskIdCounts : [0..#numLocales] atomic int;
2 forall e in hypergraph.getEdges()
3   with (var tid : int = taskIdCounts[here.id].fetchAdd(1)) {
4     var vertices = hypergraph.incidence(e);
5     ref tmp = vertices[1..#vertices.size];
6     var verticesInEdge : [1..#vertices.size] int = tmp.id;
7     processCell(new Cell(verticesInEdge), cellSets[here.id, tid]);
8 }
```

Generate power set/ASCs for the hyperedge

Boundary Matrix Computation

Step 1b: Combining K-cells

```
1 var cellSets : [0..#numLocales, 0..#here.maxTaskPar] set(Cell);
```

Hashed distribution that maps the distributed associative domains of cells to target locales

```
1 var cellSet : domain(Cell, parSafe=true) dmapped Hashed(idxType=Cell);
2 for cset in cellSets {
3   forall cell in cset with (ref cellSet) {
4     cellSet += cell;
5 }
```

Adding cells to the domain

Boundary Matrix Computation

Step 1b: Binning all K-cells

Bin cells based on their sizes

```
1 var kCellMap = new map<int, list(Cell, parSafe=true), parSafe=true>;
2 forall cell in cellSet {
3     kCellMap[cell.size - 1].append(cell);
4 }
```

Thread-safe map

Potential bottleneck: merge is happening on one Locale.

```
1 forall (_kCellsArray, kCellKey) in zip(kCellsArrayMap, kCellKeys){
2     _kCellsArray = new owned kCellsArray(kCellMap[kCellKey].size);
3     _kCellsArray.A = kCellMap[kCellKey].toArray();
4     sort(_kCellsArray.A, comparator=absComparator);
5 }
```

Sort each bin in parallel

Customized comparator for sorting

Boundary Matrix Computation: Comparator for Sorting Bins

- Customized comparator for sorting

```
1 proc Comparator.compare(a : Cell, b : Cell) : int {
2     assert(a.size == b.size);
3     for (_a, _b) in zip(a,b) {
4         if (_a > _b) then return 1;
5         else if (_a < _b) then return -1;
6     }
7     return 0;
8 }
```

Boundary Matrix Computation: What We Have Done So Far

- For example: Given a hypergraph with one hyperedge with four vertices:

```
1 [{ 0 1 2 3 }]
```

- Generate the ASCs (powerset of the hyperedge) and accumulate the k-cells in the corresponding bins:

```
1 2 -> [{ 0 1 2 }, { 0 1 3 }, { 0 2 3 }, { 1 2 3 }]  
2 1 -> [{ 0 1 }, { 0 2 }, { 0 3 }, { 1 2 }, { 1 3 }, { 2 3 }]  
3 0 -> [{ 0 }, { 1 }, { 2 }, { 3 }]  
4 3 -> [{ 0 1 2 3 }]
```

0-cells

Boundary Matrix Data Structure

```
1 class Matrix {  
2     var N : int;  
3     var M : int;  
4     var D = {1..N, 1..M} dmapped Block(boundingBox = {1..N, 1..M});  
5     var matrix : [D] int;  
6     proc init(_N: int, _M:int) {  
7         N = _N;  
8         M = _M;  
9     }
```

Block-distributed 2D array

Boundary Matrix Computation

```

1 forall |(boundaryMap, dimension_k_1, dimension_k) in zip(boundaryMaps, 0.., 1..){

  1 2 -> [{ 0 1 2 }, { 0 1 3 }, { 0 2 3 }, { 1 2 3 }]
  2 1 -> [{ 0 1 }, { 0 2 }, { 0 3 }, { 1 2 }, { 1 3 }, { 2 3 }]
  3 0 -> [{ 0 }, { 1 }, { 2 }, { 3 }]
  4 3 -> [{ 0 1 2 3 }]

  8 }

  9
10 forall |cell, colidx) in zip(boundaryMaps, 0.., 1..){

  11 1-cells
    splitKCell(ace, cell, colidx) {
      pos11s {
        pos11 {
          1 1 1 0 0 0
          2 1 0 1 0
          3 0 1 1 0
          4 1 0 0 1
          5 0 1 0 1
          6 0 0 1 1
      }
    }
  }

```

0-cells

1	1	1	1	0	0	0
2	1	0	0	1	1	0
3	0	1	0	1	0	1
4	0	0	1	0	1	1

1	1	1	0	0
2	1	0	1	0
3	0	1	1	0
4	1	0	0	1
5	0	1	0	1
6	0	0	1	1

Each column of a boundary matrix is

1;
1
1
1
1
1

Entry in the boundary matrix

Boundary Matrix Computation: What we have done so far

- Given the bins:

$1 \quad 2 \rightarrow [\{ 0 \quad 1 \quad 2 \}, \{ 0 \quad 1 \quad 3 \}, \{ 0 \quad 2 \quad 3 \}, \{ 1 \quad 2 \quad 3 \}]$
$2 \quad 1 \rightarrow [\{ 0 \quad 1 \}, \{ 0 \quad 2 \}, \{ 0 \quad 3 \}, \{ 1 \quad 2 \}, \{ 1 \quad 3 \}, \{ 2 \quad 3 \}]$
$3 \quad 0 \rightarrow [\{ 0 \}, \{ 1 \}, \{ 2 \}, \{ 3 \}]$
$4 \quad 3 \rightarrow [\{ 0 \quad 1 \quad 2 \quad 3 \}]$

- Computed the boundary maps:

0-cells		1-cells					
1	1	1	1	0	0	0	
2	1	0	0	1	1	0	
3	0	1	0	1	0	1	
4	0	0	1	0	1	1	

1	1	1	0	0
2	1	0	1	0
3	0	1	1	0
4	1	0	0	1
5	0	1	0	1
6	0	0	1	1

1	1
2	1
3	1
4	1

Computing the Smith Normal Form: Recall the Linear Algebra Operations

```
1 proc swap_rows(i, j, M) {
2     var N = M;
3     N[i, ..] <=> N[j, ..];
4     return N;
5 proc swap_columns(i, j, M) {
6     var N = M;
7     N[.., i] <=> N[.., j];
8     return N;
9 proc add_to_row(M, i, j, ri = 1, rj = 1, mod = 2) {
10    var N = M;
11    N[i, ..] = (ri * N[i, ..] + rj * N[j, ..]) % mod;
12    return N;
13 proc add_to_column(M, i, j, ci = 1, cj = 1, mod = 2) {
14    var N = M;
15    N[.., i] = (ci * N[.., i] + cj * N[.., j]) % mod;
16    return N;
```

Computing the Smith Normal Form: Recall the Linear Algebra Operations (Cont.)

```
1 proc matmultmod (M, N, mod =2) {  
2     var C : [M.domain.dim(1), N.domain.dim(2)] int;  
3     forall (i,j) in C.domain {  
4         C[i,j] = (+ reduce (M[i, M.domain.dim(2)]  
5             * N[M.domain.dim(2), j])) % 2;  
6     return C;  
7 }
```

Each entry in the resultant matrix is computed in parallel

Reduction intent: doing partial multiplications in parallel and then combining the partial sums

Putting it all together for Computing Smith Normal Form with the Basic LA Operations: LbR=S

Swapping rows/Columns

```

1 proc smithNormalForm(b) {
2     var IL = IdentityMatrix(dimL);
3     for s in 1..minDim {
4         var pivot = _get_next_pivot(s,s);
5         var rdx : int, cdx : int;
6         (rdx, cdx) = pivot;
7         if (rdx > s) {
8             S = swap_rows(s, rdx, S);
9             L = swap_rows(s, rdx, L);
10            var tmp = swap_rows(s, rdx, IL);
11            var LM = new unmanaged Matrix2D(tmp.domain.high(1),
12                                            tmp.domain.high(2));
13            LM._arr = tmp;
14            Linv.append(LM);
15        }
16        if (cdx > s) {
17            S = swap_columns(s, cdx, S);
18            R = swap_columns(s, cdx, R);
19            var tmp = swap_columns(s, cdx, IR);
20            var RM = new unmanaged Matrix2D(tmp.domain.high(1),
21                                            tmp.domain.high(2));
22            RM._arr = tmp;
23            Rinv.append(RM);
24    }

```

Potential Bottleneck !!

Adding to rows/Columns

```

1 proc smithNormalForm(b) {
2     //cont..
3     var row_indices = [idx in 1..dimL]
4         if (idx != s && S(idx,s) == 1) then idx;
5     for rdx in row_indices {
6         S = add_to_row(S, rdx, s);
7         L = add_to_row(L, rdx, s);
8         var tmp = add_to_row(IL, rdx, s);
9         var LM = new unmanaged Matrix2D(tmp.domain.high(1),
10                                         tmp.domain.high(2));
11         LM._arr = tmp;
12         Linv.append(LM);
13     }
14     var column_indices = [jdx in 1..dimR]
15         if (jdx != s && S(s,jdx) == 1) then jdx;
16     for (jdx,cdx) in zip(1..,column_indices) {
17         S = add_to_column(S, cdx, s);
18         R = add_to_column(R, cdx, s);
19         var tmp = add_to_column(IR, cdx, s);
20         var RM = new unmanaged Matrix2D(tmp.domain.high(1),
21                                         tmp.domain.high(2));
22         RM._arr = tmp;
23         Rinv.append(RM);
24     }
25
26     var LinvF = matmulreduce(Linv);
27     var RinvF = matmulreduce(Rinv, true, 2);
28     return (L,R,S,LinvF,RinvF);}

```

Opportunities for parallelization

- Straightforward: Compute SNF of all the boundary matrices in parallel.

```
1 var computedMatrices = smithNormalForm(boundaryMaps[1].matrix);
```

- Interesting case: Multiplying a list of matrices in parallel.

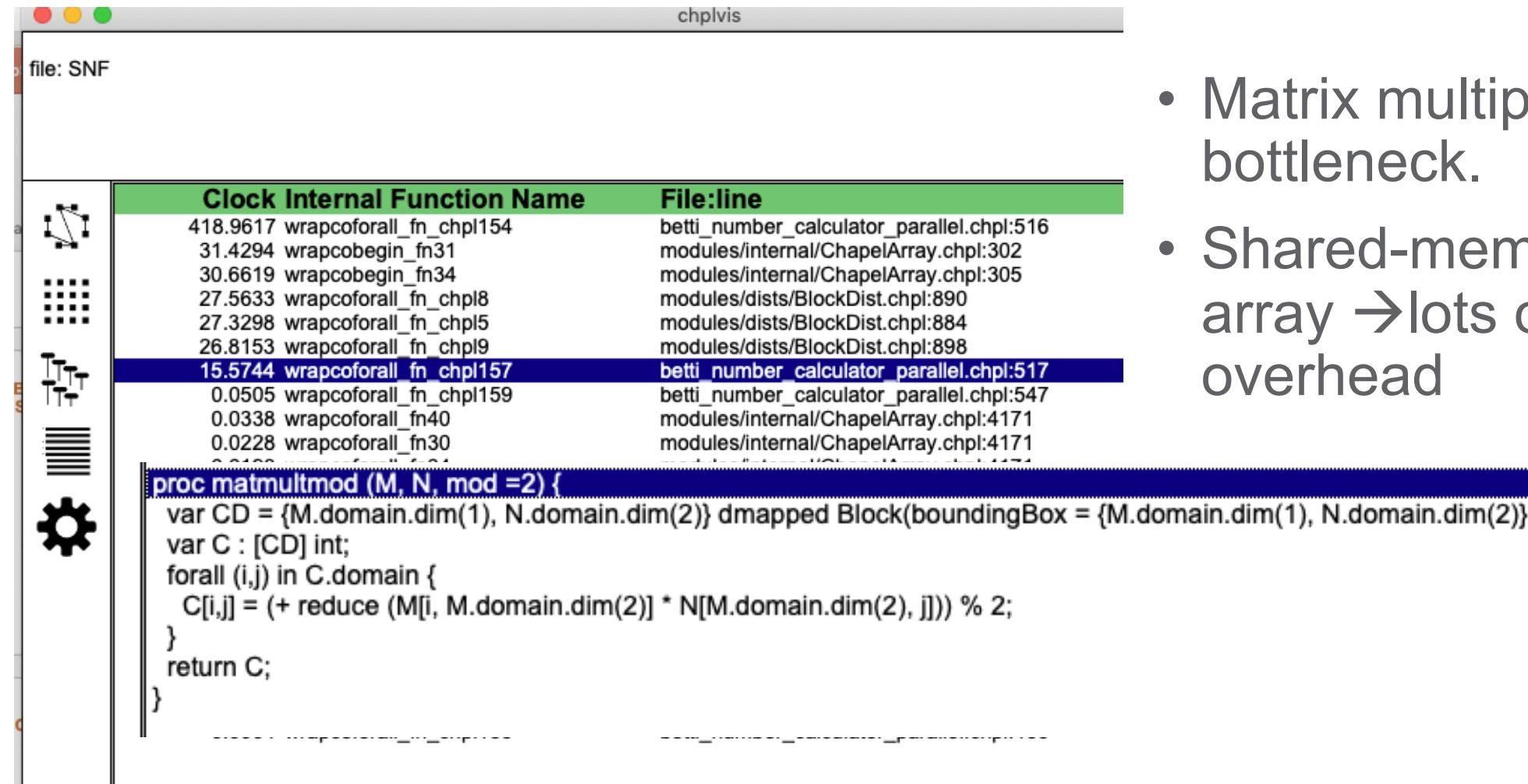
```
1 type listType = list(unmanaged Matrix?, true);
2 proc matmulreduce(arr : listType, reverse = false, mod = 2) {
3     var PD = arr[if reverse then arr.size else 1].D;
4     var P : [PD] int;
5     P = arr(1).matrix;
6     for i in 2..arr.size {
7         ref temp = matmultmod(P, arr(i).matrix);
8         PD = temp.domain;
9         P = temp;
10    }}
```

List of matrices to be multiplied

Pairwise matrix multiplication

- Reminder: What are these matrices? All the intermediate transformations done on a boundary matrix
 - Depending on the number of transformation, list-size may vary

Profiling Result



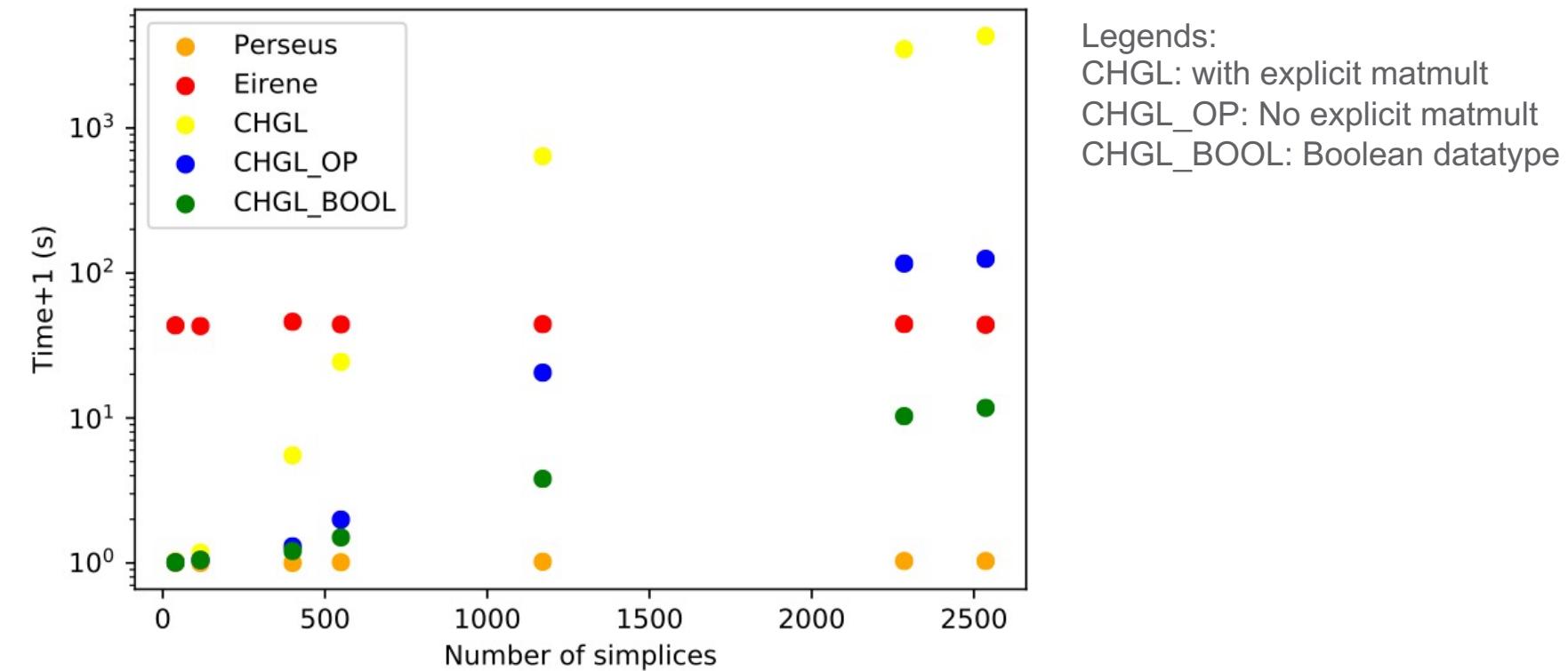
- Matrix multiplication is the bottleneck.
- Shared-memory vs distributed 2D array → lots of associated overhead
- In one of the test cases, with 20 vertices and 20 hyperedges, on one compute node/ 1 locale with InfiniBand interconnect and 20-cores, sequential execution took 25s vs distributed-memory 2D version took ~2400s !!

Algorithmic Optimizations

- Optimization 1: Reformulated the calculation of Smith Normal Form
 - Eliminate the requirement of performing explicit matrix-multiplications.
 - Instead, in-place modification of the matrices are made on-the-fly to find the invertible matrices.
- Optimization 2: Since all of our computations are done in the Z_2 field,
 - Opted for boolean datatype and operations for boundary matrices instead of integer matrices.
 - Accordingly, some of the matrix operations changed: for example `add_to_row` operation on Boolean matrix is elementwise xor.

Experimental Result

- Platform: A single compute node with a 20-core Intel Xeon processor and 132GB memory.
- Chapel version 1.20
- Compared with two other homology packages: Perseus (written in C++) and Eirene (written in Julia).



Conclusion and Future Plan

- Implemented parallel/distributed homology computation in CHGL
 - Computing the boundary matrix
 - Computing the Smith normal form (SNF) of matrices
 - Computing the reduced row Echelon form (Not shown here, similar to SNF)
- Linear algebra operations in the homology computation in Chapel
 - Concise
 - Intuitive
 - Parallel and distributed
- Bottlenecks:
 - Overhead of shared-memory vs block-distributed 2D arrays.
 - Matrix multiplication is one of the main time-consuming kernel
 - Multiplications of list of matrices need to be done in parallel.
- **Moving forward:**
 - Scalable and efficient Parallel/distributed implementation (Ongoing) and scaling test



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Thank you

