Distributed Computation of Persistent Homology

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ALENEX14
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What is persistent homology?

Turn data into growing sequence of topological spaces

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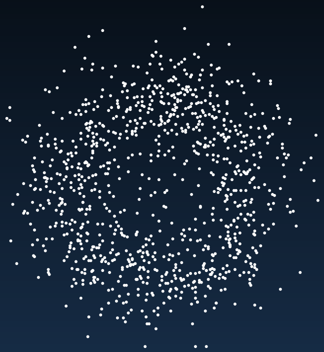

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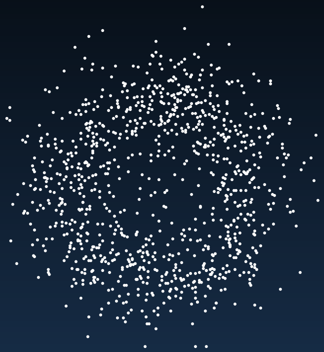

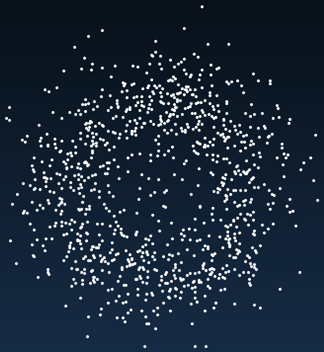

Union of balls: all points below a certain distance

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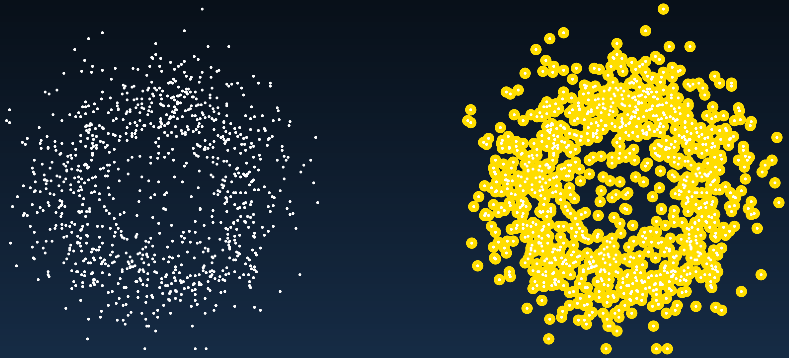

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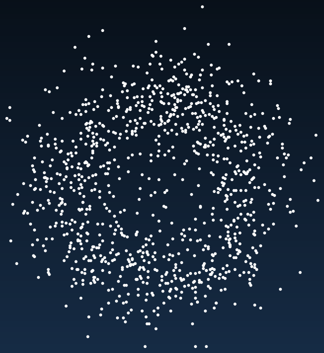

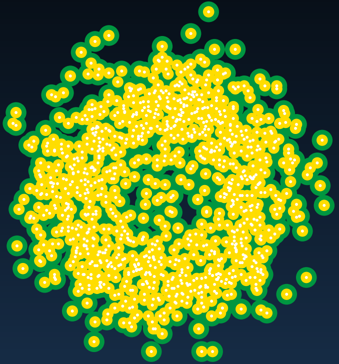

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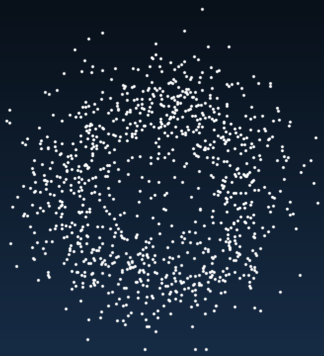

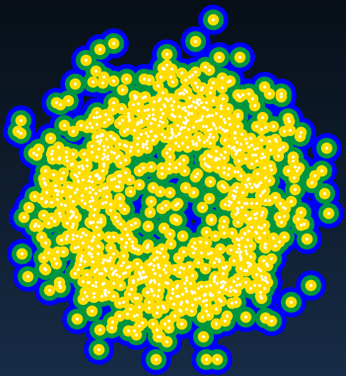

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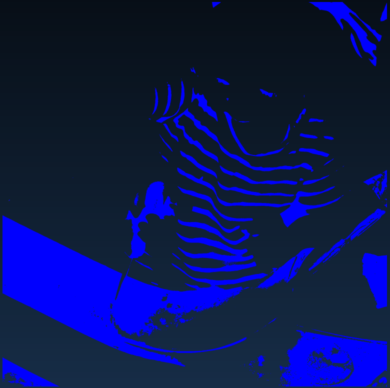

Sublevel sets: all points below a certain level

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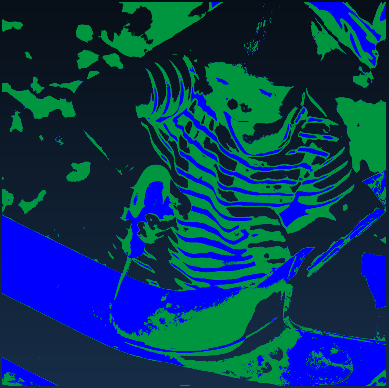

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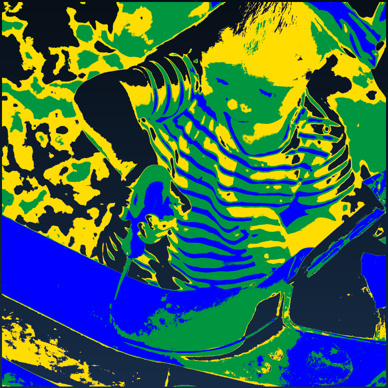

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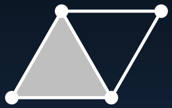

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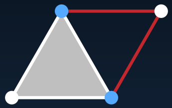

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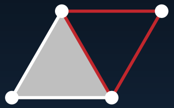

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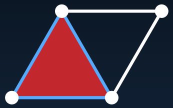

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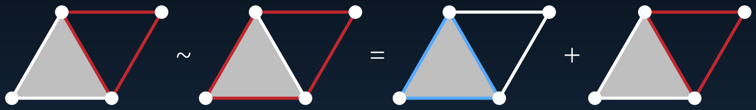

Example: filtration and boundary matrix

$D =$

	1	2	3	4	5	6	7
1			1		1		
2			1			1	
3							1
4					1	1	
5							1
6							1
7							

Matrix reduction

	1	2	3	4	5	6	7
1			1		1		
2			1			1	
3							1
4					1	1	
5							1
6							1
7							

$= D \cdot$

	1	2	3	4	5	6	7
1	1						
2		1					
3			1				
4				1			
5					1		
6						1	
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1	1						
2		1					
3			1				
4				1			
5					1		
6						1	
7							1

Pivot of column j:

- largest index with nonzero entry

Matrix reduction

	1	2	3	4	5	6	7
1			1		1		
2			1			1	
3							1
4					1	1	
5							1
6							1
7							

$= D \cdot$

	1	2	3	4	5	6	7
1	1						
2		1					
3			1				
4				1			
5					1		
6						1	
7							1

Eliminating pivot of col j:

- adding col i to col j with $i < j$ and $\operatorname{pivot}(i) = \operatorname{pivot}(j)$

Matrix reduction

	1	2	3	4	5	6	7
1			1		1	1	
2			1			1	
3							1
4					1	0	
5							1
6							1
7							

$= D \cdot$

	1	2	3	4	5	6	7
1	1						
2		1					
3			1				
4				1			
5					1	1	
6						1	
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	1	2	3	4	5	6	7
1			1		1	1	
2			1			1	
3							1
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	1	2	3	4	5	6	7
1	1						
2		1					
3			1				
4				1			
5					1	1	
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Matrix reduction

	1	2	3	4	5	6	7
1			1		1	0	
2			1			0	
3							1
4					1		
5							1
6							1
7							

$= D \cdot$

	1	2	3	4	5	6	7
1	1						
2		1					
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1	1						
2		1					
3			1			1	
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Column j is *reduced:*

- pivot of col j minimal under left-to-right column additions

Matrix reduction

	1	2	3	4	5	6	7
1			1		1		
2			1				
3							1
4					1		
5							1
6							1
7							

$= D \cdot$

	1	2	3	4	5	6	7
1	1						
2		1					
3			1			1	
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Matrix M is *reduced:*

- all columns are reduced (equivalently: pivots are unique)

Matrix reduction

	1	2	3	4	5	6	7
1			1		1		
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$= D \cdot$

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Matrix M is *reduced at index* (i, j) :

- submatrix with rows $\geq i$ and cols $\leq j$ (lower left) is reduced

Matrix reduction

	1	2	3	4	5	6	7
1			1		1		
2			1				
3							1
4					1		
5							1
6							1
7							

$= D \cdot$

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1	1						
2		1					
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4				1			
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$i = \operatorname{pivot}(j)$ and M is reduced at index $(i, j) \Rightarrow$

- column j is reduced
- (i, j) is a *persistence pair:*
  homology is created at step i and killed at step j

Matrix reduction

	1	2	3	4	5	6	7
1			1		1		
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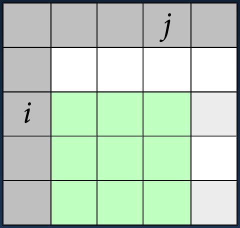
Matrix reduction in blocks

Partition $1 \ldots n$ into p *ranges:* $0 = r_0 < \cdots < r_i < \cdots < r_p = n$

Range i: $\{k : r_{i-1} < k \leq r_i\}$

- Matrix M is *reduced at block* (i, j)*:*
  submatrix of row range $\geq i$ and col range $\leq j$ is reduced



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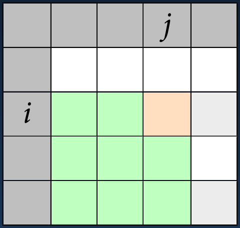
- Matrix M is *reduced at block* (i, j)*:*
  submatrix of row range $\geq i$ and col range $\leq j$ is reduced
- Matrix M is *reducible in block* (i, j)*:*
  reduced at blocks $(i, j-1)$ and $(i+1, j)$



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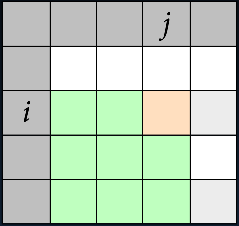

To reduce a reducible block (i, j):

- Only pivots in block (i, j) need to be eliminated
- Only cols in range j are modified
- Only reduced cols with pivot in range i are used

Distributed matrix reduction

Assign row ranges to nodes:

- Nodes collect reduced cols with pivot in their range
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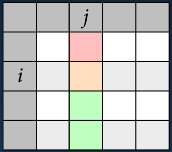

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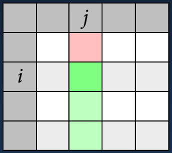

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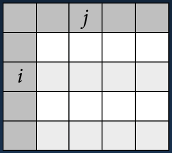

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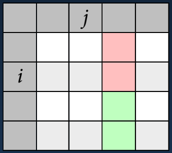

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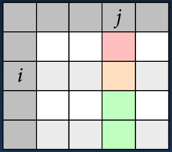

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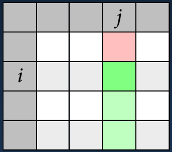

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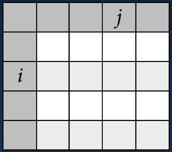

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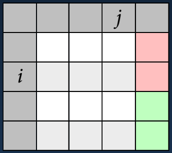

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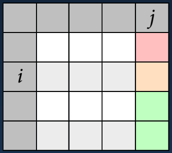

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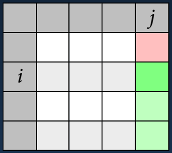

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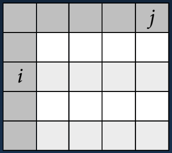

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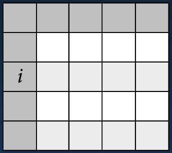


Result: node i has all reduced columns with pivot in range i

Experimental results

Running times:

	n	PHAT		DIPHA				
cores/nodes (p)		1	16	2	4	8	16	32
`GRF2-256`	1.3×10^8	15 s	5.2 s	8.9 s	5.9 s	3.0 s	2.3 s	1.5 s
`GRF1-256`	1.3×10^8	29 s	13 s	30 s	22 s	16 s	13 s	12 s
`GRF2-512`	1.1×10^9					32 s	22 s	16 s
`GRF1-512`	1.1×10^9					147 s	116 s	100 s
`vertebra16`	1.1×10^9					45 s	42 s	34 s

Peak memory consumption per node:

	PHAT		DIPHA				
cores/nodes (p)	1	16	2	4	8	16	32
`GRF2-256`	10 GB	10 GB	5.8 GB	3.0 GB	1.5 GB	0.8 GB	0.4 GB
`GRF1-256`	10 GB	11 GB	6.1 GB	3.0 GB	1.5 GB	0.8 GB	0.4 GB
`GRF2-512`					11 GB	5.5 GB	3.0 GB
`GRF1-512`					12 GB	6.1 GB	3.1 GB
`vertebra16`					14 GB	9.8 GB	5.6 GB

Experimental results

Running times:

	n	PHAT		DIPHA				
cores/nodes (p)		1	16	2	4	8	16	32
`GRF2-256`	1.3×10^8	15 s	5.2 s	8.9 s	5.9 s	3.0 s	2.3 s	1.5 s
`GRF1-256`	1.3×10^8	29 s	13 s	30 s	22 s	16 s	13 s	12 s
`GRF2-512`	1.1×10^9					32 s	22 s	16 s
`GRF1-512`	1.1×10^9					147 s	116 s	100 s
`vertebra16`	1.1×10^9					45 s	42 s	34 s

Peak memory consumption per node:

	PHAT		DIPHA				
cores/nodes (p)	1	16	2	4	8	16	32
`GRF2-256`	10 GB	10 GB	5.8 GB	3.0 GB	1.5 GB	0.8 GB	0.4 GB
`GRF1-256`	10 GB	11 GB	6.1 GB	3.0 GB	1.5 GB	0.8 GB	0.4 GB
`GRF2-512`					11 GB	5.5 GB	3.0 GB
`GRF1-512`					12 GB	6.1 GB	3.1 GB
`vertebra16`					14 GB	9.8 GB	5.6 GB

Experimental results

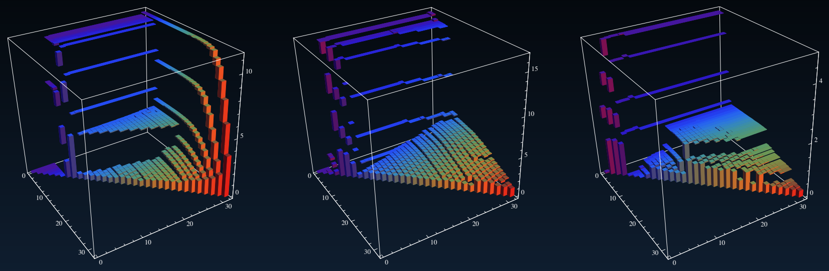
Total network transfer:

nodes (p)	2	4	8	16	32
`GRF2-256`	5.6 MB	15.1 MB	32.5 MB	67.7 MB	136 MB
`GRF1-256`	69.2 MB	218 MB	497 MB	1.0 GB	2.0 GB
`GRF2-512`			117 MB	237 MB	475 MB
`GRF1-512`			3.6 GB	7.3 GB	14.8 GB
`vertebra16`			3.3 GB	7.6 GB	15.7 GB

Maximal pairwise network transfer:

nodes (p)	2	4	8	16	32
`GRF2-256`	5.6 MB	5.6 MB	5.6 MB	6.5 MB	8.7 MB
`GRF1-256`	69.2 MB	90.3 MB	109 MB	162 MB	238 MB
`GRF2-512`			21.2 MB	21.2 MB	21.2 MB
`GRF1-512`			658 MB	658 MB	663 MB
`vertebra16`			2.9 GB	2.9 GB	2.9 GB

Running times per block



Data set `vertebra16`

- left axis: nodes
- right axis: column ranges
- vertical axis: running time
- persistence computation in dimensions 2, 1, 0

Conclusion

A fast distributed algorithm for persistent homology

- Constant (small) number of messages exchanged
- Amount of transferred data comparable to input data size
- Memory consumption scales very well
- Computation time is not an issue
- Able to compute huge instances

Source code available

- `http://dipha.googlecode.com`