Introduction to "Memory-Efficient Computation of Persistent Homology for 3D Images using Discrete Morse Theory"

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Applications and Motivations

- Protein folding and MRI scan.
- Protein folding has a exponential growth.
- MRI scan requires high cost machinery.

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Cubical Complex

A collection of vertices, edges, squares, and cubes. We refer to them as **n-d cells**.

Discrete Morse Function

A function f that assigns real numbers to cells in a cubical complex C with some rules.

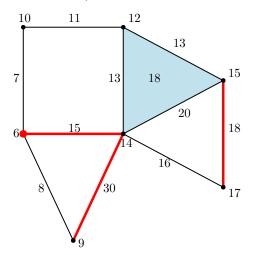
- There exists at most 1 higher-valued lower-dimensional connected vertex for an edge.
- There exists at most 1 lower-valued higher-dimensional connected square for an edge.

A cell is called **critical** if its value is smaller than all of its connected higher dimensional cells and greater than all of its connected lower dimensional cells.

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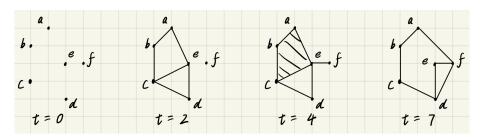
Let us look at the below example:



M-E C Persistent Homology 3D I DMT

Persistence

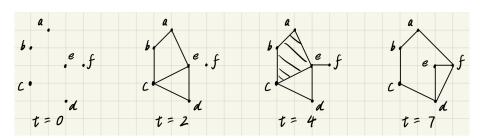
The **time difference** between the birth and death of a hole.



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Persistence

The **distance difference** between the birth and death of a hole.



Methods

- Input a 3D grey-scale image represented by array $\Omega = m \times n \times l$ and a Discrete Morse Function $f: \Omega \to \mathbb{R}$.
- Find the critical cells and compute the persistent homology.
- Use the pairs of birth and death time to construct 3D models.



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Result

Data	Size	# critical nodes	Total memory (MB)		Total time (min)	
			standard	this paper	this paper	previous
Hydrogen	128 imes 128 imes 128	30,409	528	35	1.15	0.62
Christmas Present	$246 \times 246 \times 221$	6,544,279	3367	496	23.46	266.78
Foot	$256 \times 256 \times 256$	2,044,799	4224	434	305.79	2.85
Molecule	$1120\times1131\times1552$	2,082,895	494967	31950	313.38	*

Table: Comparative between this paper and an earlier algorithm.



Possible Improvements

Time complexity

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References



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