HW3 - Code Description - Apr12, 2025

Optimization/data structure choices and performance.

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This is a brief description about "`va.VR`" Julia Module that I developed borrowing interface/partial implementation of Simplex Tree `\Hodge` package, which is not exported by Hodge module for external use and does not do any realization (expand to larger complexes as higher filtration radius is used). Entire program runs from same "`coding_assignemnt.jl`" `Simplicial Sets + Gluing` approach. Keeping track of orientations turned out to be the "`KEY`" for running multiple filtrations across 2 input-files in short enough duration to create persistence barcode diagrams for H0, H1, H2 homologies.

> **Point 1: Datastructures/Otimizations**
>
> Simplex Tree makes ordering of lower level simplices redundant. BOISSONNAT and MARIA (2020):
>
> (a) Union-find in Julia implemented path-halving in sep 2024.
>
>   (i) IntDisjointSets, ACSet (used in Simplicial Set) do not allow for incremental building of Simplicial Complex as described in Zomorodian (2010), however there is an even better approach compressing dense complexes accesses described in RIESER (2024). I deployed 2-way reduction. First create an array describing simplex of desired dimension or below (going upto 5 was very expensive unless I did filtration in simplex tree as suggested by Antonio Rieser to save accesses), saving only highest dimesnion ones in va.VR module using simplex tree. Then send this to coding_assignemnt.jl for further reduction by not even adding removing triangles of +, -ve orientations if that face is shared as 1234 and 1235 are added for shared face 123. This alone reduced by triangle count from 320,000 triangles to 96000 triangles.
>
>   (ii) After realizing that these complexes are dense and fully connected, I reduced a cube with 6 tetrahedrons to 1 tetrahedron as I was only going to compute homologies upto H2 and as we discussed, one can reduce fully connected and filled tetrahedron to a point as there are no topological properties there. This reduced my triangle count to 16969 from 96000 at filtration diameter of 10.00.
>
> (b) gathersimplices in VR.jl implements first half of collection using simplex tree defined in ST.jl (from Hodge + my edits).
>
> (c) Loop starting at line 608: in coding_assignment.jl implements second half of collection filtering dense structures to 3d level.

Plot.jl then plots barcode using PersistenceDiagram Julia package providing *PersistenceInterval*, *PersistenceDiagram* data-structures with basic plotting support. See PersistenceDiagram.jl for details.

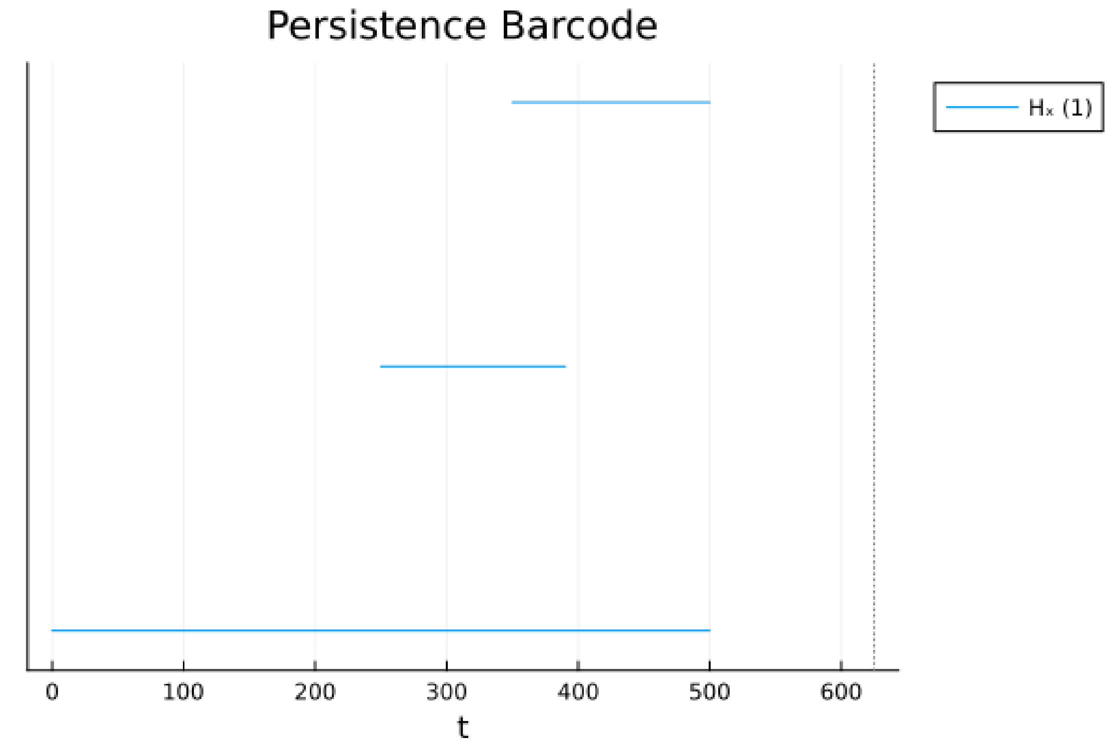
Point 2: Outcomes

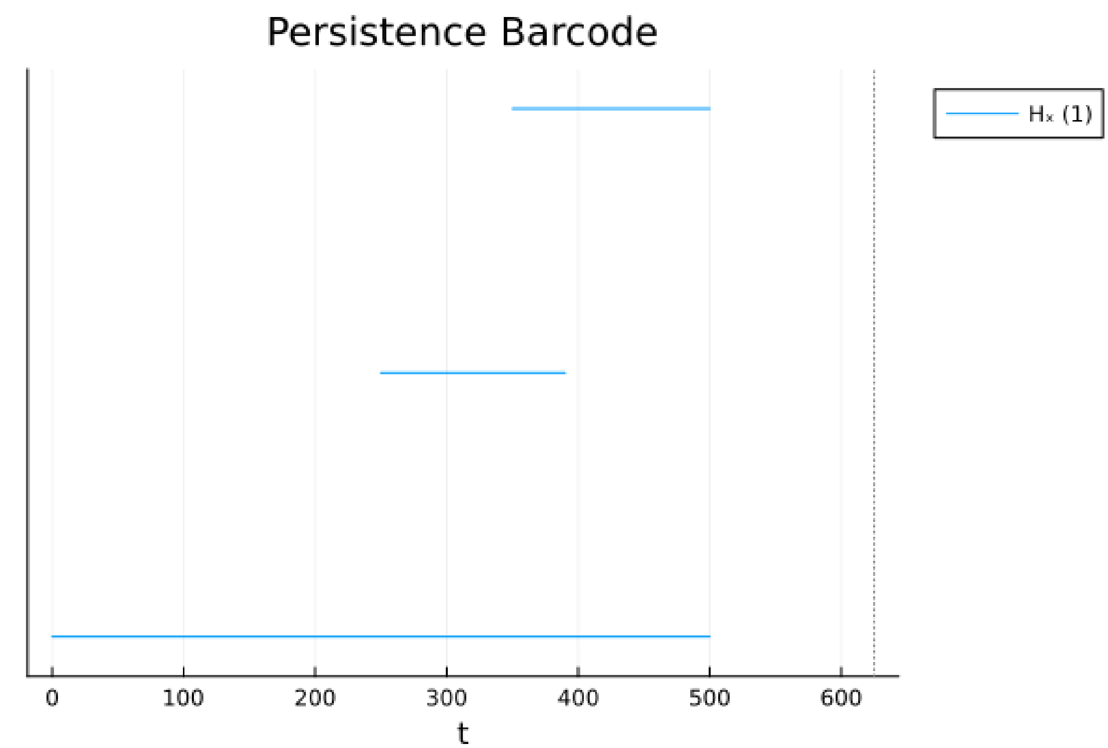
This is an example problem taken from **?**:

(a) Prove the following

  (i) Outcomes for CDHWdata_5.txt
  (ii) diam = 2*r is used for filtration.
  (iii) r = 1.5 :V = 93, :E = 0, :Tri = 0, :Tet = 0
  (iv) r = 2.5 :V = 93, :E = 80, :Tri = 4, :Tet = 0
  (v) r = 3.5 :V = 93, :E = 566, :Tri = 1308, :Tet = 34
  (vi) r = 3.9 :V = 93, :E = 852, :Tri = 3097, :Tet = 56
  (vii) r = 5.0 :V = 93, :E = 1819, :Tri = 16969, :Tet = 494
  (viii) h0 = [93, 31, 1, 1, 1]
  (ix) h1 = [0, 4, 3, 0, 0]
  (x) h2 = [0, 0, 803, 2281, 14748]
  (xi) x = [3, 5, 7, 7.8, 10] – Filtrations
  (xii) persistence_5.png
  (xiii) Outcomes for CDHWdata_3.txt
  (xiv) diam = 2*r is used for filtration.
  (xv) r = 1.5 :V = 93, :E = 0, :Tri = 0, :Tet = 0
  (xvi) r = 2.5 :V = 93, :E = 84, :Tri = 20, :Tet = 0
  (xvii) r = 3.5 :V = 93, :E = 542, :Tri = 1130, :Tet = 25
  (xviii) r = 3.9 :V = 93, :E = 853, :Tri = 3146, :Tet = 64
  (xix) r = 5.0 :V = 93, :E = 1861, :Tri = 18198, :Tet = 609
  (xx) h0 = [93, 31, 1, 1, 1]
  (xxi) h1 = [0, 5, 0, 0, 0]
  (xxii) h2 = [0, 0, 660, 2321, 15770]
  (xxiii) x = [3, 5, 7, 7.8, 10]
  (xxiv) persistence_3.png
  (xxv) This is also available in Plot.jl. As filtration diameters go up, higher dimensional structures begin to appear subsuming lower dimensional ones. H1 (1 dimensional holes appear at filtration diameter 5 and disappear by filtration diameter by 7.8. Input files 3 and 5 do show this difference for H1 homology.

(b) $\cdots$





Lowest bar is H0 homology, middle bar is H1 homology (t is doubly loaded - normally simplices will get subsumed by incremental construction and with increasing filtration, more edges/complexes will get connected allowing for further consolidation. I printed this whole even for dataset 3 (UPPER) and dataset 5 (LOWER) in one picture.

Above barcode diagrams could not be converted to diagonal diagrams using plane PersistenceDiagrams package as it only supplies data structures for other more sophisticated packages.

There are 2 program outputs "`program_run.txt`" and "`program_output.txt`". Program_run.txt shows how various simplices, if accepted without any pre-processing will simply overwhelm the LinearAlgebra system (note in program also talks about as to why RREF is better than smith, in terms of performance).

There are numerous other optimizations which are easy to implement but are not yet implemented. One is edge collapsing as edges are added to simplex tree, by just saving long paths. Julia also provides persistent arrays which can just allow for only saving δ change in data-structures such as lists.

One thing that is not yet checked is making sure *Cayley Megner Determinant* is positive as Euclidean guarantee does not hold once all point of tetrahedron are on hyperbolic syrfaces. See Cayley Magner Determinant and Veljan (1995)

As without this property of realizability of distance matrix, one can not construct simplicial complex. Using SchHifli determinant Veljan (1995).
K = 1 (spherical)   det C > O
K = O (Euclidean)   det C = O
K = -1 (hyperbolic)   det C < O

References

BOISSONNAT, J.-D. and MARIA, C. (2020). *THE SIMPLEX TREE: AN EFFICIENT DATA STRUCTURE FOR GENERAL SIMPLICIAL COMPLEXES*. arXiv.

RIESER, A. (2024). *A NEW CONSTRUCTION OF THE VIETORIS-RIPS COMPLEX*. arXiv.

Veljan, D. (1995). *The Distance Matrix for a Simplex*. CROATICA CHEMICA ACTA.

Zomorodian, A. (2010). *Fast construction of the Vietoris-Rips complex*. ScienceDirect.