Topological processing of biomedical images

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Research Proj.: MTM2016-81030-P: Topological Recognition of 4D digital images via HSF model
Topology = Mathematics of Connectivity
Mathematics of Relations

Computational Topology. Analysis and Representation.
Methodology and goals

• Methodology: “Radical” rethinking of topological notions in order to design parallel algorithms for topological computing of objects embedded in $\mathbb{R}^n$.

• Engineering strategy: **Big Data into Huge Bitopological Scenario.** To represent “big data” into a much more sparse and topologically structured “huge” scenario as an special symmetric pair of dynamical system. One (non-unique) Top-Model of the data will be an assymetric pair of dynamical systems “bitopologically equivalent” to the previous one, such the number of sinks or attractors is (or is closed to) the minimal one. Within this scenario, parallel topological computing takes place.

• Our general goal: To obtain efficient lossless (or near-lossless) compression coding of the original data, also allowing topological parallel processing within compressed domain.
Combinatorial setting: Primal-dual abstract cell complex (pdACC)

- An abstract cell complex $\text{ACC} = (E, B, \text{dim})$ is an abstract set $E$, $B$ is an asymmetric, irreflexive and transitive binary relation called the bounding relation among the elements of $E$ and $\text{dim}$ is a function assigning a non-negative integer to each element of $E$ in such a way that if $B(a,b)$, then $\text{dim}(a) < \text{dim}(b)$.


- An primal-dual abstract cell complex $\text{ACC} = (E, B_p, B_d, \text{dim})$ is an abstract set $E$, $B_p$ and $B_d$ are asymmetric, irreflexive and transitive binary relations called resp. primal and dual bounding relations among the elements of $E$ and $\text{dim}$ is a function assigning a non-negative integer to each element of $E$ in such a way that if $B_p(a,b)$, then $\text{dim}(a) < \text{dim}(b)$ and $B_d(a,b)$, then $\text{dim}(a) > \text{dim}(b)$.

Note: A “geometric” cell complex is in a natural way a primal-dual abstract cell complex being the bounding relation $B_p$ (“to belong to the boundary of”) dual of $B_d$ (“to belong to the coboundary of”). In this context, we can talk about the homology and cohomology derived from $B_p$ and $B_d$, respectively.
HUGE BITOPOLITICAL SCENARIO FOR BIG DATA

Cell subdivision strategy

Working at combinatorial level.

Incomplete picture within the connectivity graph.

**Symmetric primal-dual ACC**

Explosion of the size of the topology computation space

WHAT FOR??

**Coboundary (dual)**

**Boundary (primal)**

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*Fig. 1* a) A cell complex $K$ with four 0-cells (1, 2, 3, 4), four 1-cells (a, b, c, d) and one 2-cell (A).

b) The connectivity graph $G(K)$. 
Abstract cell complex (III)

- Representing 2D digital images using pACC
  - Pixel = PE
    - Periodic in $\mathbb{R}^2$
    - Face = 2-cell
    - Cross = 1-cell
    - Point = 0-cell

PE: processing element
pACC (IV)

PE: processing element

Symmetric pACC in $\mathbb{R}^2$

Cell dim. and Primal bounding in $\mathbb{R}^2$

Cell dim. and Dual bounding in $\mathbb{R}^2$
pACC (V)

Cell dim. and primal bounding in $\mathbb{R}^3$ (dual bounding are inverse)

R3 processing element
pACC (VI)

• Primal (resp. dual) vector \((c', c'')\) with multiplicity \(B^p(c', c'') \neq 0\)

• Open star of \(c\): \(c\) and all \(c'\) such that \(B^p(c', c'') \neq 0\)

• Color of \(c\): pure foreground, pure background, mixed

• A primal (resp. dual) crack associated to the \(i\)-cell \(c\):
  • Primal \((c; c')\), plus Dual vector
pACC (V)

• Primal \textit{pACC-homotopy operation} $Op^p$
• Tree compression or contraction.
Parallel Algorithm for computing a HSF of a pACC

**Input**: A uniquely dimensional symmetric pACC; List of cells.

**for each** dim
  **for each** cell c
    **if** exist c’ in Star(c) with Primal Bounding (c, c’) = 1 **then**
      Apply Primal pACC-homotopy operation Op to c, c’
    **end if**
  **end for**
  Define new cracks
  Collect incidence graph of this dim.

**Outputs**: Incidence graph (dense skeleton) of every dim.
A HSF (Homological Spanning Forest) as generalization of a classical Connected Component Labeling based on spanning forest of all the vertices of a graph.


Ambiance-based parallel strategies for computing HSF of digital objects

Main motivation: combinatorial optimization algorithms in logarithmic time!!!!

Two visual interpretations of homology chain-integral complexes of the contractible 2D euclidean cubical tiling


Topological tree of a binary 2D image

Parallel algorithm based on ambiance for computing a HSF: Combinatorial optimization based on transport through the flow

Processing element (PE): two possible states
Only two activation states for primal vectors

Only crack transports going West or South

MrSF  HSF
### Table 1: Timing results in seconds for medical images of different size of http://goldminer.arrs.org/top-40.php, using an Intel Xeon E5 2650 server.

<table>
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<tr>
<th>Thumbnail Name at goldminer top40</th>
<th>#threads</th>
<th>AJNR2013</th>
<th>AJR2004</th>
<th>EURORAD2015</th>
<th>AJR2009</th>
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<tr>
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<tr>
<td># sources after south and west transports</td>
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<td>Max # of hops along the MrSF-0-tree</td>
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**Fig. 20.** Timing results in seconds for medical images of different size of http://goldminer.arrs.org/top-40.php, using an Intel Xeon E5 2650 server.

**Fig. 14.** Statistical data using the first 8 available medical images of http://goldminer.arrs.org/top-40.php

**Fig. 21.** Speedup for the medical images of previous Figure 20 vs the number of threads.
The case of 2D images (V)

- Timing results not good for only one processor
- Simplified HSF 3x slower than fastest CCL (Connected Component Labeling)
- But very good scalability: Maybe the fastest CCL alg. if using lots of processors
Fig. 1. A ring perpendicular to Y axis with an associated MrSF.
Pipeline of the algorithm

Time orders of HSF computation of a $m_1 \times m_2 \times m_3$ image (supposing lots of processors). $s_{01}$ and $s_{12}$ are the number of sequential cancellations of remaining 0/1 and 1/2 cells resp.
Adjacency Trees of 3D Images

# CC = 1
# TUNNELS = 2
# CAVITIES = 1

# CC = 1
# TUNNELS = 2
# CAVITIES = 1

Adjacency Tree: ADJT
Adjacency Tree in 3D

Fig. 7. HSF of a sphere with two external handles. The colors code is the same as the employed for the previous figures. All trees are being displayed along with their corresponding critical cells. In the upper right part of the figure, a red link represents the BG CC of the image.

Experimental Results and Conclusions

1. Firstly synthetic Menger sponges were used to test the parallel algorithm by comparing the outputs with the classical ones.

2. For small random images (up to 15x15x15) the proposed method was almost perfect: HSF was completed in a fully parallel manner for almost 100% of the tested images.

3. For 30x30x30 B/W random images (50/50 density)
   - Counting sequential transport iterations of 0/1 cell pairs
   - Counting sequential transport iterations of 1/2 cell pairs

4. For three trabecular bone images of sizes 43x43x9, 64x64x13, and 43x43x9: similar results
## Experimental Results

<table>
<thead>
<tr>
<th>FG critical 0-cells (MrSF)</th>
<th>Initial critical cells</th>
<th>After 1(^{st}) transports of 0/1 cells</th>
<th>After 2(^{nd}) transports of 0/1 cells</th>
<th>After 3(^{rd}) transports of 0/1 cells</th>
<th>After 4(^{th}) transports of 0/1 cells</th>
<th>After sequential transports of 0/1 cells</th>
<th>After parallel transports of 1/2 cells</th>
<th>After sequential transports of 1/2 cells (final MrSF)</th>
<th>Percentage of parallel transports in the 1(^{st}) transport (0/1 cells)</th>
<th>Percentage of parallel transports (0/1 cells)</th>
<th>Percentage of parallel transports (1/2 cells)</th>
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<td>1510.60</td>
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<td>31</td>
<td>75.58</td>
<td>91.49</td>
<td>97.14</td>
</tr>
</tbody>
</table>
Experimental Results and Conclusions

• An algorithm for computing homological (co)holes of nD-images
  • A pure combinatorial optimization process
  • Based on a dense topological skeleton (HSF-structures)
• Almost fully parallel algorithm
  • Intrinsic parallelism (identical processing at each PE)
  • Theoretical timing order: $O(\log(\sum m_k))$
  • Only a linear term less than the 0.5% of the total amount of voxels (even for random images).

• Future work
  • Relationships between homological holes (HSF region-adjacency-graph)
  • Topological pattern recognition based on HSF information.
  • 4D version of the algorithm
Muchas Gracias!
Some topologizations within digital context

Different 22 unit-cell complexes associated to point pattern subsets using 26-adjacency (3D Lego)


Computer Graphics aftermath: Topological Marching Cube (Kenmochi & Imiya)
4D-cellularization


402 patterns up to isometry polyhedra associated to configurations of four points within the Unit 4d-cube


Configurations in the elementary 4D cube with three marked vertices
Fractal topology?

Visualization of tunnels in different levels of recursivity of the Menger sponge

HSFs for measuring fractal topology

Validation of our HSF-based strategy in well-known fractal topologies

Theorem 1. For the number $T_n$ of tunnels of the $n^{th}$-recursion polyhedral Menger Sponge $\mathcal{M}_n$, we have that

\[
T_1 = 5 \\
T_n = 8 \cdot T_{n-1} + [T_{n-1} - 2 \cdot (8^{n-2} + 8^{n-3} + \ldots + 8 + 1)] \cdot 12 + 5 \\
= 20 \cdot T_{n-1} - 24 \cdot (8^{n-2} + 8^{n-3} + \ldots + 8 + 1) + 5
\]