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DA2791

1 mensaje

Discrete Applied Mathematics <dam@elsevier.com> 18 de noviembre de 2013 04:42
Para: sbdani@us.es

Ms. Ref. No.: DA2791
Title: Cell Complexes and Membrane Computing for Thinning 2D and 3D Images
Discrete Applied Mathematics

Dear Professor Díaz-Pernil,

Please see our referee comments on your manuscript. You may view any uploaded reports and additional information on the paper by logging in to the EES website. Please go to http://ees.elsevier.com/dam/ and login as an Author with the following:

Your username is: sbdani@us.es

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As you will see, based on these comments, the publication of your paper will, unfortunately, not be possible.

Hoping for a more positive outcome next time, and thanking you for your interest in our journal, I remain,

Yours sincerely,

Endre Boros
Editor-in Chief
Discrete Applied Mathematics

Reviewer comments:

Reviewer #1: In my opinion the paper does not fit a journal such as discrete applied mathematics. In fact no theorem is given. Furthermore the paper is a complex reformulation of an algorithm which can be expressed in a concise way (39 rules are needed to describe the algorithm). In this context, it is not clear at all what is the interest of such an approach.

Reviewer #2:
*Combining/using different computational methods can be very interesting BUT the combination needs to be motivated or justified somehow. I find nothing of that in this paper (speed, ease of implementation, comparison to other methods etc.). I think this paper lacks a clear (any) motivation and evaluation - why/how is this approach better or important.

*As a reader I wonder what I would gain/benefit from this approach. It seems to require quite a bit of work to set up all the rules and steps in the computation. I think you should discuss the number of rules and the work to set them up.

*Based on the ref list you already seem to have shown the bridging between membrane computing, cell complexes and image analysis on other standard image analysis methods. This paper comes across a little as just another method with the same approach. (again you need to motivate and compare to other approaches)

*I think you should relate this to the wide skeletonization/thinning literature/field in more detail than just refer to an overview article: what skeletons(surface and/or curve skeletons) are produced in 3D , how does this compare to other skeletonization/thinning approaches (based on e.g., cell complexes)? Can it be extended to gray-scale?

*It would be nice with some illustrations and examples.

*Figure 1 (left) is wrong (the collapsing bits are missing).

*There are a few (not so many) strange sentences and spelling errors.

Reviewer #3: This is one of the few pioneering papers that try to explore the potentially rich intersection of image processing and membrane computing. This paper presents a membrane computing model for a recent and promising thinning algorithm by Liu et al. [1], largely based on topological concepts, i.e. cell complexes. The first part of the paper is well written and, following Kaczynski et al. [25], makes a better presentation of required topological concepts than Liu et al. [1] and its uncited published version [1b].

[1b] Liu et al., A simple and robust thinning algorithm on cell complexes, Pacific Graphics 2010, 29 (2010), 7.

Towards the end, the presentation seems to lose focus and is less readable. The membrane computing model and its proof are hard to assess. That's often inevitable for complex algorithms, but it can probably made better.

I think that this paper can be published, after the authors make a series of improvements, as suggested in the list below (not sorted in importance order).

6.39: Please clarify if this is weak or strong priority

10.Fig 1: The left image is missing a lot

10.26-31: The definition of the star operator should probably be omitted, as it does not seem to be anywhere used and only complicates the reading

10.37-39 This is a good place to identify both members of a simple pair: facet (which actually could be defined, more generally, as a maximal face) and the terminal cell, introduced only at 11.45-46 (its definition could be moved near the facet definition)

10.39-40: "does not change the topology", suggestion to be more precise, i.e. homotopy equivalence, or, in this case, simple homotopy equivalence

1. 55-56: (footnote, major issue) " In the original work by Liu, [1], the thinning algorithm is designed for cell complexes of any kind, however we restrict to cubical complexes." This is an important aspect and should be mentioned much earlier, maybe even in the abstract or at least in the introduction, certainly not in a footnote!

Extending the given membrane system from cubical complexes to more general cell complexes seems a daunting task, definitely not trivial!

Minor suggestion: remove the comma in "Liu, [1]"

12.Alg 1: Here I have two major issues.

A) The original paper [1b] specifically mentions that "It is tempting to combine the two tasks, computing MP and retaining cells, within a single pass. However, retaining cells during thinning may have an impact on the MP values of other cells computed at later iterations.". Then, they decide against this and split the whole task into two separate passes; actually, in the end, their algorithm has three distinct steps.

Alg. 1 amalgamates all these three steps into a single one. Have the authors assessed (theoretically or

experimentally) that this does not adversely affect the output? At least a good discussion is needed.

B) The original paper [1b] clearly indicates that "If a simple cell has multiple facets [read faces] that are candidates as witness facets [read terminal free faces], an arbitrary one is selected."

However, Alg. 1 does not make such a choice, instead, it seems to prune all terminal faces that pass the filters. Most likely, this will affect the topological properties of the complex (its homotopy type).

The authors need to consider this very carefully.

12. Alg. 1, 19: (minor issue) \pi_2 is not defined (but could be understood for most readers)

13: 2k-adjacency, shouldn't it be 2^k-adjacency? Note that for k=3, this means 8-adjacency. Are these two k's the same: (a) k as the spatial dimension of the space and (b) k as an adjacency indicator?

13.41-42: in the formula, it is not clear which quantifier applies to p: exists or forall?

13.55-56: (major issue, footnote) "The reader is supposed to be familiar with concepts of Image Algebra. For a detailed text, see [27]. In particular, a *reset* is the generalization of pixel from 2 to n dimensions"

The paper makes detailed presentations of reasonably well known concepts, e.g. CW complexes, but suddenly assumes that readers are familiar with more niche concepts and terminology. I don't expect that many people are familiar with the term *resel*. Moreover, the indicated text [27] does not contain any occurrence of *resel*. The best definition I found starts with "Resel = 3D Resolvable Element" and it does not map 1:1 on pixels or voxels. So, a few more details are needed here

14: the encoding of cubical complexes takes a bit too long and seems to require a simple example, e.g. how all faces of the unit cube are encoded

14.42: "for one in a complex" -> "for one dimension in a complex" ?

14.5: "the cubical cell built" -> "the cubical cell complex built"

14.56: where does m come from?

19.30: "we will proof" -> "we will prove" or (better) "we prove"

Section 5: needs an intuitive explanation of the inner working of the presented P system; a well-chosen simple example and some intuitive traces or diagrams might help a lot

22: "Algebraic Topology..." suggestion to use lower case letters only (this applies to the whole paper, not only here)

Section 6: The authors should also discuss the benefits of using membrane computing models, for both domains (membrane computing and image processing).

The authors should briefly present some of the results of their model and compare these with Liu t al. results. Are these identical or not and why? Also, comparative actual runtime performances would be interesting, if available (cf. 4.20)

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