View Reviews

Paper ID
534

Paper Title
Biologically-Constrained Region Merging for Connectome Reconstruction

REVIEWER #1

REVIEW QUESTIONS

1. Paper Summary. What is the paper about? Please, be concise (3 to 5 sentences)
The paper introduces a novel pipeline to reduce segmentation errors in connectome reconstructions. This graph-based method receives in input a skeleton constructed from the connectome segmentation and combines 3D convolutional neural networks (CNN) and a multicut algorithm to specifically address "split errors", i.e. wrong cuts of single neuronal processes, by embedding ad-hoc biological constraints.

2. [Paper Strengths] Please discuss, justifying your comments with the appropriate level of details, the strengths of the paper (i.e. novelty, theoretical approach and/or technical correctness, adequate evaluation, clarity, etc). For instance, a theoretical paper may need no experiments, while a paper with a new approach may require comparisons to existing methods.
The strength of the paper lies in several aspects. First, the authors tackle the problem of improving connectome reconstructions starting from the segmented image, making the proposed method less sensitive to the acquisition system and the used reconstruction algorithm. Second, the proposed pipeline makes a smart use of 3D CNN to embed and exploit ad-hoc biological constraints. Third, the end-to-end solution requires a rather limited amount of "relatable" parameters to be tweaked by the user. Fourth, the manuscript contains a wealth of experiments covering almost any aspect of the pipeline. Fifth, all the pipeline components are usually well explained in the text and illustrations. Sixth, the paper is equipped with a section about the computational performance of the various components, which allows the reader to better evaluate the opportunity of using such a pipeline.

3. [Paper Weaknesses] Please discuss, justifying your comments with the appropriate level of details, the weaknesses of the paper (i.e. lack of novelty – given references to prior work-, lack of novelty, technical errors, or/and insufficient evaluation, etc). Note: If you think there is an error in the paper, please explain why it is an error. Also remember that theoretical results/ideas are essential to ECCV (some theoretical papers may not need to have experiments). If the theory is novel and interesting, but the results did not outperform other existing algorithms, it is not necessarily a reason to reject. It is not appropriate to ask for comparisons with unpublished papers and papers published after the ECCV deadline. In all cases, please be polite and constructive. ECCV 2018 policy on dual submission and arxiv appears in the guidelines.
In my opinion, the most prominent weakness of this work is the disproportion between complexity of the method and the gain in terms of reconstruction accuracy: it is a bit disappointing that such clever pipeline, combining some heavy "machinery" (despite the reasonable computational efficiency), yields just an 9% increase in accuracy compared to baseline. Moreover, the authors do not specify whether this improvement can be considered relevant and whether follow-up quantifications would effectively be more reliable if operating on data processed with the proposed method rather than without this step.

4. Recommendation
Probable Accept

5. [Preliminary Evaluation] Please indicate to the AC, your fellow reviewers, and the authors your current opinion on the paper. Please tell the ACs what points you think have the most weight in your reviews and summary, and why.

Despite some minor flaws listed above, I overall appreciated the novelty of the paper, its clarity and the wealth of experiments to benchmark individual or chains of components of the proposed pipelines. This approach will certainly spark the interest of the people working in the field of connectome reconstructions and probably even beyond this community.

I think the paper should be accepted for the following reasons:
1) A novel graph-based method is introduced to reduce a source of error in connectome reconstructions, that has not been really addressed before.
2) The method is almost completely independent on the acquisition scheme used to collect the raw data.
3) There is a smart use of 3D CNN operating on the segmentation to generate biologically meaningful weights for the edges of the multicut algorithm employed at the end.
4) The method was trained on a dataset and validated on a completely different one.
5) There is a wealth of experiements benchmarking all the individual components of the pipeline.
6) There is a limited amount of parameters to be tweaked by the user.
7) The ideas described in this paper could be re-used for other applications and imaging datasets.

6. [Rebuttal Requests] Please list here a few crucial items that should be addressed in the rebuttal
I would like to ask to the authors to address the following two points.
1) Discuss how relevant is the gain in accuracy provided by the proposed method in relation to the final quantification goals or biological questions to be addressed.
2) I found unclear the description of the input for the 3D CNN in the subsection "Edge probability" of section 3.2. Did I understand correctly that the CNN operates on 3D ROIs of the baseline segmentation and that the selection of the ROIs is based on the skeleton endpoints? How can a voxel belong at the same time to two different segments of the skeleton? Should we assume that the cases where the channels are set to -0.5 are complementary to those for which the channels are set to +0.5, which are indicated in the text? In this regard, I think it would be extremely helpful for the readership to enrich the text of this subsection with an explanatory figure/plot similar to those already present in the manuscript, that greatly help to understand the complex issues under discussion.

7. Confidence
Confident. I understand the issues in this paper but am not an expert.

REVIEWER #2

REVIEW QUESTIONS

1. Paper Summary. What is the paper about? Please, be concise (3 to 5 sentences)
The paper suggests an instance segmentation pipeline for connectomics data. Superpixels are skeletonized, and a merge probability for any pair of proximate endpoints is estimated. On the resulting edge-weighted graph, a lifted multicut problem is solved approximately. The resulting segmentation is made cycle-free in a heuristic manner.

2. [Paper Strengths] Please discuss, justifying your comments with the appropriate level of details, the strengths of the paper (i.e. novelty, theoretical approach and/or technical correctness, adequate evaluation, clarity, etc). For instance, a theoretical paper may need no experiments, while a paper with a new approach may require comparisons to existing methods.
* Interesting problem

* Well-written paper, easy to reproduce (especially given that authors pledge to make code available)

* The edge probability estimation network ingests only an indicator volume of local superpixel shapes, making it invariant against staining methods

3. [Paper Weaknesses] Please discuss, justifying your comments with the appropriate level of details, the weaknesses of the paper (i.e. lack of novelty – given references to prior work-, lack of novelty, technical errors,

or/and insufficient evaluation, etc). Note: If you think there is an error in the paper, please explain why it is an error. Also remember that theoretical results/ideas are essential to ECCV (some theoretical papers may not need to have experiments). If the theory is novel and interesting, but the results did not outperform other existing algorithms, it is not necessarily a reason to reject. It is not appropriate to ask for comparisons with unpublished papers and papers published after the ECCV deadline. In all cases, please be polite and constructive. ECCV 2018 policy on dual submission and arxiv appears in the guidelines.

* Not clear why a skeleton representation is helpful in the graph generation. The edge weights in the graph are anyway estimated from a volumetric (not skeletonized) representation of local superpixel memberships.

* The network estimating merge probabilities ingests a representation of local superpixel shape that is not very rich: an indicator vector is used to indicate if a voxel belongs to one or the other or none of the superpixels involved. Such a winner-takes-all representation, if unaccompanied by some measure of uncertainty, or some representation of the raw data, is not rich. This is the flipside of the third "strong point" mentioned above.

* No comparison with state of the art. Authors argue that their data used for evaluation is larger than any of the data sets used in public benchmarks. Even so, results on those public benchmarks should be given.

* The lifted multicut problem is solved only approximately; it would be good to know how much this impacts the quality of the solution.

* The acyclicity constraint seems to be built not into the lifted multicut solver, but applied as a greed (and suboptimal) postprocessing step.

* Not clear on which graph and edge weights Dijkstra's algorithm (for estimation of long-range affinities) operates.

4. Recommendation

Borderline

5. [Preliminary Evaluation] Please indicate to the AC, your fellow reviewers, and the authors your current opinion on the paper. Please tell the ACs what points you think have the most weight in your reviews and summary, and why.

The fundamental merit of the skeletonization for the task at hand is unclear to me, and I await clarifications in the rebuttal.

6. [Rebuttal Requests] Please list here a few crucial items that should be addressed in the rebuttal

Please clarify the fundamental advantage of working with skeletons, given that the actual representation used for estimation of edge weights is volumetric. The only use of skeletons then seems to be in identifying edges for the graph over which lifted multicut is solved.

Please compare to state of the art on public benchmarks.

The indicator vectors used for superpixel 1 vs 2 are arbitrary. Please explain how you taught the network to become invariant with respect to their permutation.

7. Confidence

Very Confident. I am an expert in this field.

REVIEWER #3

REVIEW QUESTIONS

1. Paper Summary. What is the paper about? Please, be concise (3 to 5 sentences)

This paper introduces a region merging method for introducing biological constraints in connectome segmentation. A preliminary segmentation is assumed (normally a CNN/U-net based pixel classifier for cell boundaries and some initial merging of superpixels obtained from it). The resulting preliminary segmentation is skeletonized with an existing algorithm. Cubic volumes of the resulting geometrical structures around potential merges are scored by a 3D CNN to give edge weights between segments. A multi-cut segmentation using the above edge weights is performed.

2. [Paper Strengths] Please discuss, justifying your comments with the appropriate level of details, the strengths of the paper (i.e. novelty, theoretical approach and/or technical correctness, adequate evaluation, clarity, etc). For instance, a theoretical paper may need no experiments, while a paper with a new approach may require comparisons to existing methods.

+ Meaningful improvement in accuracy over two large datasets

3. [Paper Weaknesses] Please discuss, justifying your comments with the appropriate level of details, the weaknesses of the paper (i.e. lack of novelty – given references to prior work-, lack of novelty, technical errors, or/and insufficient evaluation, etc). Note: If you think there is an error in the paper, please explain why it is an error. Also remember that theoretical results/ideas are essential to ECCV (some theoretical papers may not need to have experiments). If the theory is novel and interesting, but the results did not outperform other existing algorithms, it is not necessarily a reason to reject. It is not appropriate to ask for comparisons with unpublished papers and papers published after the ECCV deadline. In all cases, please be polite and constructive. ECCV 2018 policy on dual submission and arxiv appears in the guidelines.

- Very specialized to a particular biological image analysis problem.
- Missing references to important related work on biological priors for connectome reconstruction Krasowski et al, Neuron Segmentation With High-Level Biological Priors, IEEE TMI 2018
- I think the term "constraints" is misleading. The CNN learns soft scores for plausible biological geometries, not hard constraints.
-How the global constraints are introduced in the multi-cut framework is not adequately described. How is the tree-topological constraint enforced (lines 272-278)? There is no description of this.

4. Recommendation

Borderline

5. [Preliminary Evaluation] Please indicate to the AC, your fellow reviewers, and the authors your current opinion on the paper. Please tell the ACs what points you think have the most weight in your reviews and summary, and why.

This paper introduces a 3D CNN to score merges between adjacent segments of a graph for connectome segmentation. Meaningful improvement is shown on two large connectome datasets. The paper states that the publicly available challenge datasets are too small to show meaningful improvement. Unfortunately, because of this, we are not able to compare the approach to many other algorithms for connectome segmentation. This point coupled with the fact that this is a very specialized application might make the paper less interesting for the ECCV audience.

6. Confidence

Confident. I understand the issues in this paper but am not an expert.