3D Segmentation for Connectomics

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Abbreviation:	seg-3d
Number of instances:	2
Number of variables:	7958, 101220
Number of labels:	7958, 101220
Number of factors:	291460, 4343230
Order:	2
Function type:	Potts

Description Connectomics is a long-term effort in computer vision and neurobiology to automatically reconstruct neural circuits from large volume images [2, 1, 3, 4].

This benchmark includes the two graphical models that have been used in [1] to partition 3D images of 10^9 voxels into a previously unknown number of segments, based on a learned likelihood of merging adjacent supervoxels. The images were acquired at different laboratories using different electron microscopy techniques.

Objective / Learning For the purpose of this benchmark, these models are provided in their dual form in which there is one variable x_v for every supervoxel $v \in V$. Every variable can assume as many labels as there are supervoxels, i.e. labels $0, \ldots, |V| - 1$.

For every pair $\{v, w\} \in E$ of supervoxels which are neighbors in the supervoxel adjacency graph (V, E), there is one second-order term

$$\varphi_{vw}(x_v, x_w) = \begin{cases} \theta_{vw} \in \mathbb{R} & \text{if } x_v \neq x_w \\ 0 & \text{otherwise} \end{cases} \quad . \tag{1}$$

The parameters θ which can be positive or negative are differences of log-likelihoods that are learned independently from empirical training data as described in [1]. There are no first-order terms in the objective function

$$J(x) = \sum_{\{i,j\} \in E} \varphi_{ij}(x_i, x_j) \quad . \tag{2}$$

References

[1] Bjoern Andres, Thorben Kröger, Kevin L. Briggman, Winfried Denk, Natalya Korogod, Graham Knott, Ullrich Köthe, and Fred A. Hamprecht. Globally optimal closed-surface segmentation for connectomics. In *ECCV*, 2012.

[2] Björn Andres, Ullrich Köthe, Thorben Kroeger, Moritz Helmstaedter, Kevin L. Briggman, Winfried Denk, and Fred A. Hamprecht. 3D segmentation of SBFSEM images of neuropil by a graphical model over supervoxel boundaries. *Medical Image Analysis*, 16(4):796–805, 2012.

[3] Jan Funke, Bjoern Andres, Fred A. Hamprecht, Albert Cardona, and Matthew Cook. Efficient automatic 3D-reconstruction of branching neurons from EM data. In *CVPR*, 2012.

[4] Amelio Vazquez-Reina, Daniel Huang, Michael Gelbart, Jeff Lichtman, Eric Miller, and Hanspeter Pfister. Segmentation fusion for connectomics. In *ECCV*, 2011.