SSHMT: Semi-supervised Hierarchical Merge Tree for Electron Microscopy Image Segmentation

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Summary
• Quick background: region-based methods after pixel-based membrane detection improve accuracy for neuron segmentation in electron microscopy (EM) images
• Goal: learn scoring function for region merging with few training samples
• Contributions: extend existing hierarchical merge tree (HMT) framework with:
  • An unsupervised loss term that enforces structural consistent predictions about region merging
  • A Bayesian model for probabilistic semi-supervised learning and automatic parameter estimation
• Result: with 3% to 7% of labeled data, consistent performance close to supervised HMT with full labeled sets

Hierarchical Merge Tree
• Start with over-segmenting initial superpixels, build a merge tree
• Learn to score potential merges: boundary classifier
• Infer final segmentation

Unsupervised Constraint
• Consistency constraint: no merge after split in leaf-to-root path
  • In disjunctive normal form: let \( f_i \) be merge indicator
  • Ex: \( F = \nabla_i \ast (N_i^{-1} f_i \wedge \nabla_i^{-1} f_i) \) is true iff consistent
  • Real-value approximation: let \( f_i \in [0, 1] \) be boundary classifier prediction
    \[ \bar{F} = 1 - \Pi_i (1 - f_i \cdot \Pi_i (1 - f_i)) = 1 \] iff consistent

Semi-supervised HMT
• Goal: learn a boundary classifier whose predictions minimize \( \|1 - \bar{F}\| \) for any tree path
  • Boundary classifier: \( f_{\text{bd}}(x) = 1 / (1 + \exp(-w^Tx)) \)
  • Bayesian model to learn \( f_{\text{bd}} \):
    \[ P(w) \propto P(w) \cdot P(1|w, \sigma_w) \cdot P(y_i|w, \sigma_y) \propto \exp \left( \frac{||w||^2}{2} \right) \]
• Objective function:
  \[ f(w, \sigma_w, \sigma_y) = \frac{1}{2} \|w\|^2 + \frac{1}{2\sigma^2} \|1 - \bar{F}_w\|^2 + N_w \log \sigma_w + \frac{1}{2\sigma^2} \|y_i - \bar{F}_w\|^2 + N_y \log \sigma_y \]
• Gradient descent on \( w \); alternately estimate \( \sigma_w \) and \( \sigma_y \) using closed-form solutions to \( \partial f / \partial \sigma_w = 0 \) and \( \partial f / \partial \sigma_y = 0 \)
• Infer final segmentation as in HMT

Results
• Datasets: mouse neuropil (2D SBFSEM, 700×700×700), mouse cortex (3D STEM, 1024×1024×1024), and Drosophila (3D FIBSEM, 500×500×500)
• Randomly subsample labeled data for as supervised data; all samples as unsupervised data; repeat 50 times whenever possible
• Evaluation metrics: adapted Rand error (lower is better)
• Quantitative results are shown in Fig. 2; qualitative results are shown in Fig. 3 and 4.

Fig. 1: Toy example of (a) initial superpixels, (b) a merge tree, and (c) a final segmentation

Fig. 2: Means (curves) and standard deviations (bars) of adapted Rand errors using different amount of labeled supervsised data. (X-axis: log-scale amount of labeled samples, Y-axis: adapted Rand error, Red: HMT, Blue: SSHMT)

Fig. 3: Examples of 2D segmentation for the mouse neuropil dataset, including (a) original EM images, (b) HMT and (c) SSHMT results using 1 labeled image as supervised data, and (d) corresponding ground truth images

Fig. 3: Examples of 3D segmentation for the Drosophila dataset, including (a) HMT and (b) SSHMT results using 12 (6.25%) labeled cells as supervised data and (d) the corresponding ground truth cell segments