Efficient Correction for EM Connectomics with Skeletal Representation

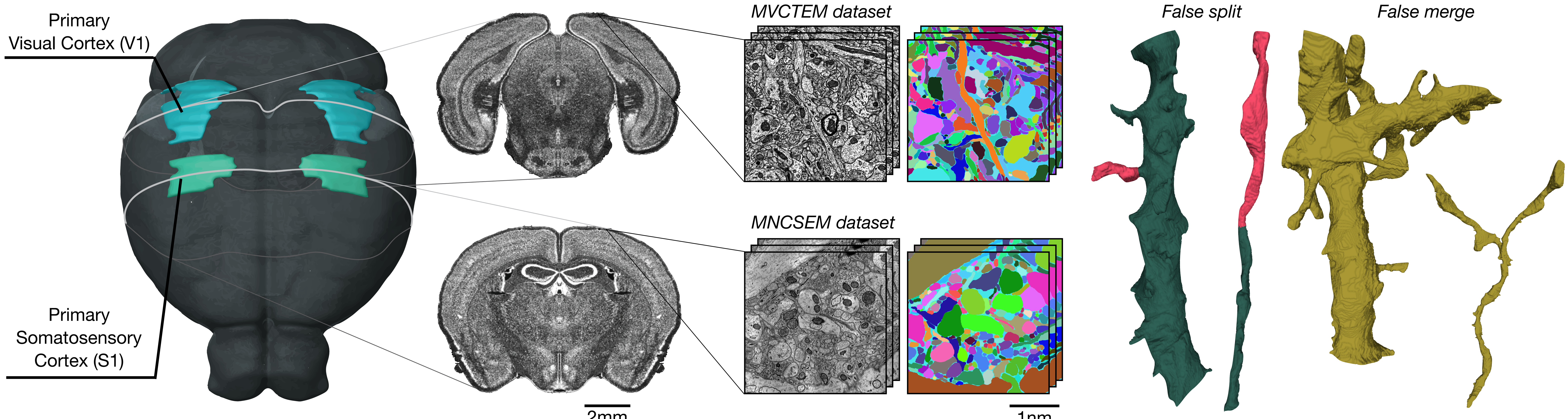
Konstantin Dmitriev[1,2], Toufiq Parag[2], Brian Matejek[2], Arie E. Kaufman[1,2], Hanspeter Pfister[2]
[1]Stony Brook University, NY, USA; [2]Harvard University, MA, USA

Stony Brook University

HARVARD John A. Paulson School of Engineering and Applied Sciences

Introduction

The cellular structure of the nervous system is complicated. Connectomics aims to reconstruct the wiring diagram of the mammalian brain at nanometer resolution segmenting the stacks of electron microscopy (EM) images. Given the tremendous amount of data, computational solutions are required. Despite advances, current solutions retain false merge and false split errors. We present an efficient correction algorithm of the initial EM segmentations.

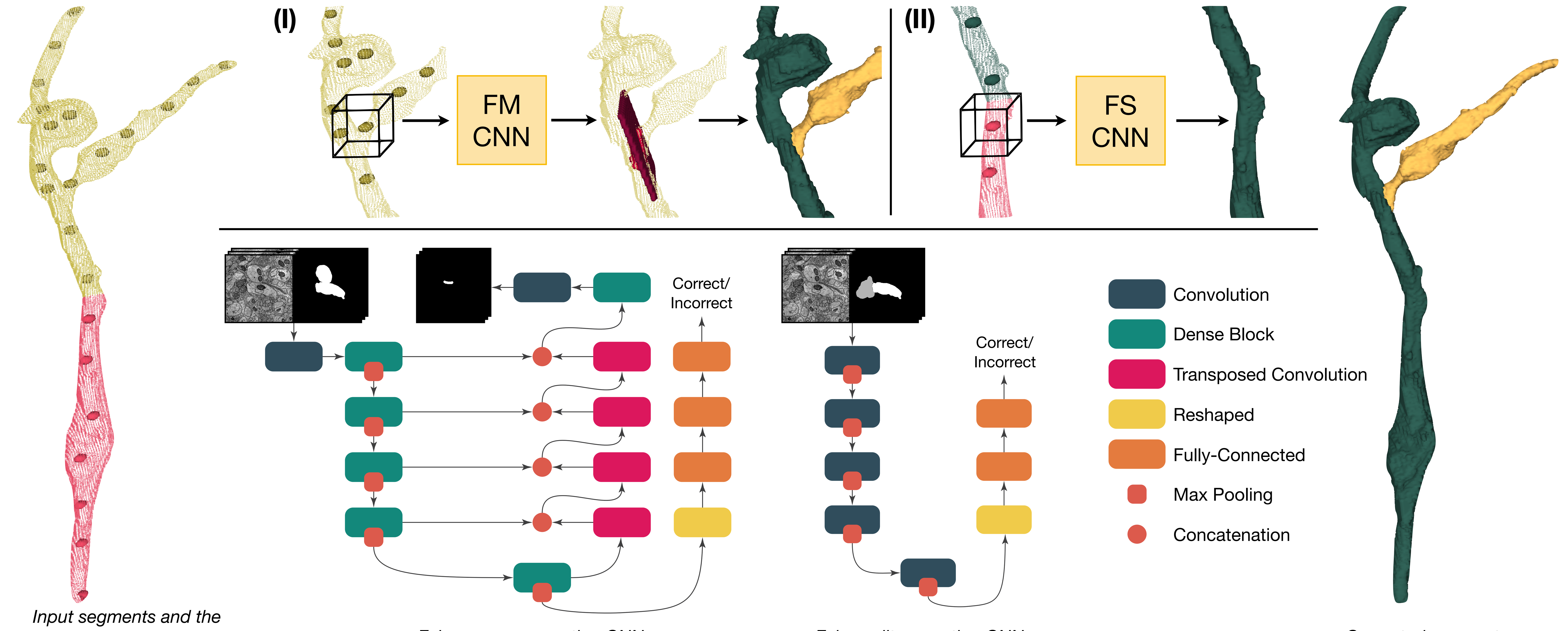


Mouse brain

3D examples of incorrect segmentations

Method

Our algorithm consists of two successive stages: (I) false marge (FM) and (II) false split (FS) corrections. Each stage exploits skeletal joints of the segments within the input segmentation. Utilizing skeletal joints significantly reduces the number of search locations and thus enables our method to be scalable to petabyte scale reconstruction.



Input segments and the skeleton joints

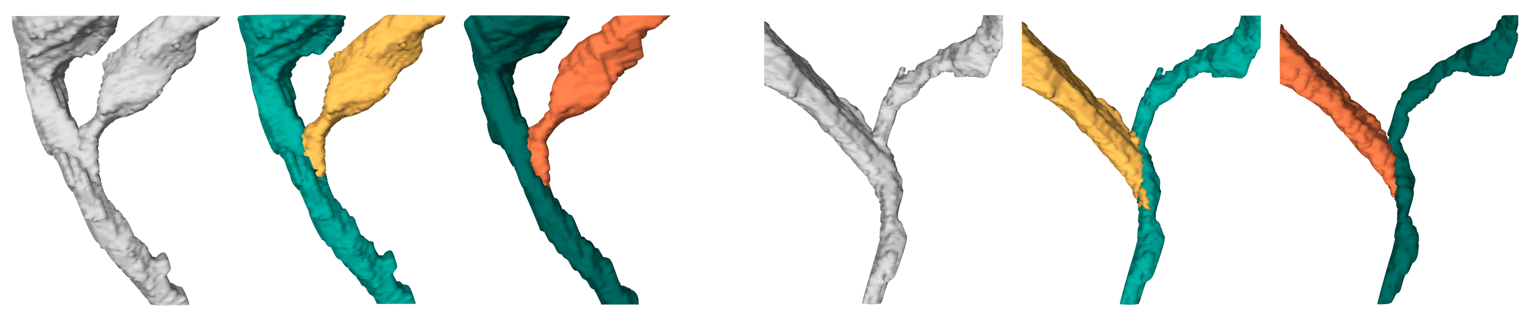
False merge correcting CNN

False split correcting CNN

Corrected segment

Results

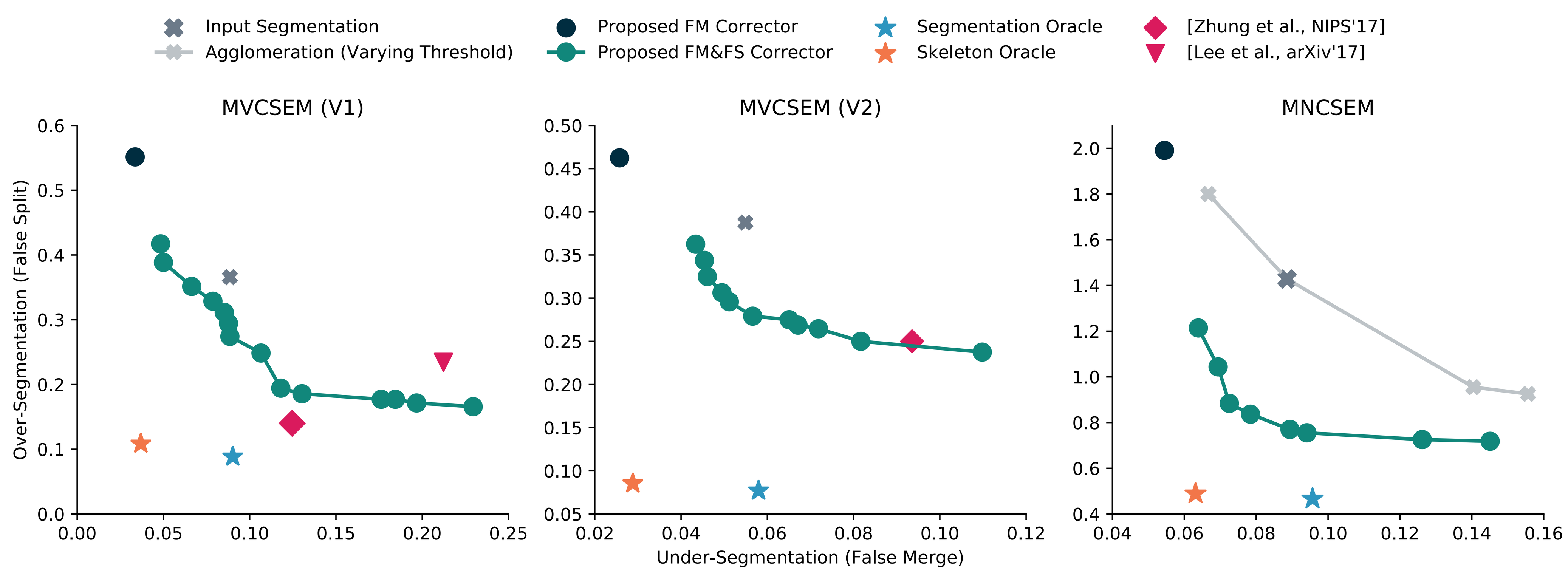
We trained and evaluated our method on the Mouse Visual Cortex TEM (MVCTEM) and Mouse Neocortex SEM (MNCSEM) datasets.



3D examples of the input, corrected and ground truth segmentations

	MVCSEM (V1)	MVCSEM (V2)	MNCTEM
Volume size (voxels)	1.07×10^9	1.07×10^9	0.816×10^9
Query points (skeleton joints)	40621	41513	62815

Search space reduction



VI curves for different experiments

Acknowledgment

The authors gratefully acknowledge Jonathan Zung, Sebastian Seung of Princeton Neuroscience Institute, NJ and Clay Reid, Allen Institute for Brain Sciences, WA for sharing their results with us. This research has been partially supported by the National Science Foundation grants IIS1447344, IIS1527200, IIS1607800, NRT1633299, CNS1650499, the Intelligence Advanced Research Projects Activity (IARPA) via Department of Interior/Interior Business Center (DoI/IBC) contract number D16PC00002, the Marcus Foundation, and the National Heart, Lung, and Blood Institute of the NIH under Award Number U01HL127522. The content is solely the responsibility of the authors and does not necessarily represent the official view of the NIH. Additional support was provided by the Center for Biotechnology, a New York State Center for Advanced Technology; Cold Spring Harbor Laboratory; Brookhaven National Laboratory; the Feinstein Institute for Medical Research; and the New York State Department of Economic Development under contract C14051.