

## **A Bottom-Up Approach for Pancreas Segmentation Using Cascaded Superpixels and (Deep) Image Patch Labeling**

### **Abstract:**

Robust organ segmentation is a prerequisite for computer-aided diagnosis, quantitative imaging analysis, pathology detection, and surgical assistance. For organs with high anatomical variability (e.g., the pancreas), previous segmentation approaches report low accuracies, compared with well-studied organs, such as the liver or heart. We present an automated bottom-up approach for pancreas segmentation in abdominal computed tomography (CT) scans. The method generates a hierarchical cascade of information propagation by classifying image patches at different resolutions and cascading (segments) superpixels. The system contains four steps: 1) decomposition of CT slice images into a set of disjoint boundary-preserving superpixels; 2) computation of pancreas class probability maps via dense patch labeling; 3) superpixel classification by pooling both intensity and probability features to form empirical statistics in cascaded random forest frameworks; and 4) simple connectivity based post-processing. Dense image patch labeling is conducted using two methods: efficient random forest classification on image histogram, location and texture features; and more expensive (but more accurate) deep convolutional neural network classification, on larger image windows (i.e., with more spatial contexts). Over-segmented 2-D CT slices by the simple linear iterative clustering approach are adopted through model/parameter calibration and labeled at the superpixel level for positive (pancreas) or negative (non-pancreas or background) classes. The proposed method is evaluated on a data set of 80 manually segmented CT volumes, using six-fold cross-validation. Its performance equals or surpasses other state-of-the-art methods (evaluated by “leave-one-patient-out”), with a dice coefficient of 70.7% and Jaccard index of 57.9%. In addition, the computational efficiency has improved significantly, requiring a mere 6 ~ 8 min per testing case, versus  $\geq 10$  h for other methods. The segmentation framework using deep patch labeling confidences is also more numerically stable, as reflected in the smaller

performance metric standard deviations. Finally, we implement a multi-atlas label fusion (MALF) approach for pancreas segmentation using the same data set. Under six-fold cross-validation, our bottom-up segmentation method significantly outperforms its MALF counterpart:  $70.7 \pm 13.0\%$  versus  $52.51 \pm 20.84\%$  in dice coefficients.

