SLIC in a defined mask with applications to medical imaging

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Abstract. Supervoxel methods are effective for reducing an image or volume into a set of locally similar regions which has a number of advantages to pixel based methods for segmentation and graph based methods. Simple linear iterative clustering (SLIC) is an effective supervoxel method but is limited to rectangular volumes. In this paper we reformulate the SLIC algorithm to work more effectively in predefined regions-of-interest. The key contribution is the reformulation of the seed point initialisation. This method is applied to an example image with source code and a live demo available. There are a number of applications to computing SLIC inside an mask region including assessment of pathological subregions.

1 Introduction

Supervoxel oversegmentation methods are effective for reducing an image or volume into a set of locally similar and spatially related regions. This reduces the redundancy of the image, speeds up processing and, therefore, makes complex analysis of regional relationships more feasible. Simple linear iterative clustering (SLIC) [1] has been shown to be a fast and effective method of generating superpixels/supervoxels.

A key issue with SLIC is that it is designed for rectangular regions (images or volumes) but may not effective for generating supervoxels within masked regions, for example, an organ or tumour, due to the grid seed-point initialisation. This issue is compounded if the mask is irregular.

Supervoxel methods have a number of potential applications in subregion analysis, particularly in medical imaging. These subregions may be defined inside a delineated region such as an organ or region of pathology. We propose a number of small modifications to the SLIC method to generate robust supervoxels within a defined region-of-interest instead of a rectangular region. A demonstration of maskSLIC method is available at: maskslic.birving.com and example code can be found at https://github.com/benjaminirving/maskSLIC.git.

2 Masked simple linear iterative clustering

SLIC performs a local clustering into \( k \) supervoxels of roughly equal size [1]. This is initialised by seed points on a regular grid, where the grid interval is given
by $S = \sqrt{N/k}$ and $N$ is the number of pixels in the image. SLIC performs a local $k$-means clustering in a $2S \times 2S$ region around each seed point, each pixel is assigned to a cluster centre and the cluster centre is updated. The distance term is defined by spatial and feature contributions:

$$D = \sqrt{\left( \frac{d_c}{m} \right)^2 + \left( \frac{d_s}{S} \right)^2}$$

(1)

where $d_c$ and $d_s$ are the euclidean distances between the feature and spatial vectors, respectively with $m$ as a weight. As $m$ increases the supervoxels become more regular as they the spatial contribution becomes higher.

As shown in Fig 2 a-b) the ordinary SLIC grid initialisation means that the points are unevenly distributed within the mask, which affects supervoxel generation, due to the spatial localisation of the method.

We propose modifications to the SLIC method to work within any defined ROI. Steps are taken to generate improved initialisation points within an ROI, and, once the points are initialised, the clustering is limited to voxels inside the ROI.

**Step 1** Given the number of required supervoxels ($n$), a distance transform is used iteratively place seed points the maximum distance from the boundaries and other seed points (Figure 2c-f). Therefore, any new point is placed at the location furthest from any other point or the boundaries. The distance transform $D_i(p)$ at iteration $i$ and position $p$ can be calculated as follows:

$$D_i(p) = \min_{q \in G} (d(p, q) + 1(q))$$

(2)

where

$$1(q) = \begin{cases} 0, & \text{if } p \in P \\ \infty, & \text{otherwise} \end{cases}$$

(3)

and the optimal location of the point is:

$$p_i = \arg\max_p D_i(p)$$

(4)

**Step 2** $S$ is redefined as the mean distance between pairs of closest points instead of the grid distance.

**Step 3** SLIC is initially applied to the seed points with only the distance feature ($d_s$ from Eqn 1) to improve the the optimal centroids given the shape of the mask (Figure 2g).

$$d = d_s$$

(5)

**Step 4** Finally, the conventional formulation of SLIC is applied but is restricted to voxels that are defined inside the mask (figure 2h).

This seeding method shares some of the goals of $k$-means++ [2] for improved and robust seeding of $k$-means. In our case we have an explicitly defined region for supervoxelisation using SLIC and so can define optimal seed locations.
Fig. 1: Initialising SLIC seed points inside a mask. a) and b) show the original SLIC formalation. c-e) Show the distance transform heat map for iteratively placing each seed points, f) shows the seed points placed using the distance transform, g) shows the points using spatial local clustering and h) shows the final SLIC supervoxels (image is CC0 with no copyright restrictions from photographer Stefan van der Walt).
We extend this maskSLIC formulation to 4D perfusion images using the principal component decomposition of perfusion for supervoxelisation as outlined in [3] and [4]. Therefore, a tumour region can be decomposed into spatially contiguous subregions with similar perfusion as shown in Figure 2.

Fig. 2: 3D supervoxels extracted from a 4D DCE-MRI scan

3 Discussion

We propose a method to define the SLIC supervoxels inside an arbitrarily defined region to extend SLIC beyond image based subregion extraction. The four steps show the modifications that are required to adapt the standard supervoxel approach. Figure 2 is an example of the difference that is achieved by using this method for a defined region. There are a number of potential applications including as a preprocessing method to analyse pathological regions in medical imaging.

References

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