GlandVision: A Novel Polar Space Random Field Model for Glandular Biological Structure Detection

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Tissue diagnosis is an important part of modern day medicine. Where disease is suspected, tissue samples can be taken from the patient and viewed under the microscope by a Pathologist. In many human tissues, cells are organized into complex anatomical units called *glands*. In many disease states the glands are disrupted, often in a characteristic fashion. If automated image analysis is to be used to facilitate tissue diagnosis, then recognition of glands is essential.

A typical microscopic image of the human colon and the glands contained in it are shown in Fig.1. It can be seen there that a gland is composed of a group of cells who sit side-by-side and form the boundaries. Depending on the way the tissue has been sectioned, the shape of a gland can vary hugely and this poses significant challenge to computational algorithms for automatic gland detection.

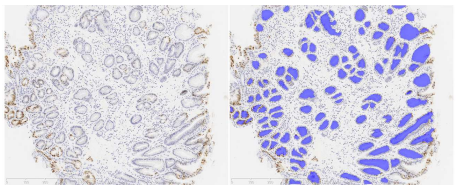

Figure 1: (a) A microscopic image of human colon tissue containing glands. (b) The glands are manually annotated in blue solid color as shown in the right image.

In this paper, we propose a novel method for detecting those glandular structures. We noticed that one of the most distinctive properties of a gland is that they usually exhibit a closed shape structure. If we place our viewpoint inside the gland, we will see a closed contour, which means if we place the co-ordinate's origin inside a gland and transform the gland to the polar space, we will see a continuous line structure along vertical direction in the polar image. Some examples are shown in Fig.2. It is seen that if the origin is inside a gland, we can see an obvious line structure in their corresponding polar image (e.g., regions circled as A, B, and C); if the origin is outside a gland there is no such line structure in its polar image (e.g., the region circled as D). Based on this observation, the problem of detecting glands can be formulated as the problem of detecting those line structures in the polar image.

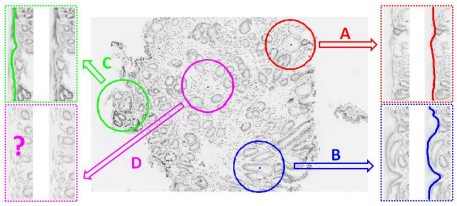

Figure 2: A, B and C correspond to cases where the polar space's origin is inside a gland while D corresponds to the case where the polar space's origin is not inside a gland. We can clearly see a continuous line structure in A, B and C, while this kind of structure can not be seen in D.

To detect the gland contours in the polar image, we developed a Conditional Random Field (CRF) model [2]. We assign each row of the polar image a label Y_i, which indicates the position of the gland contour at each row. The graphical model of our CRF contains only 360 nodes in total and is illustrated in Fig.3.

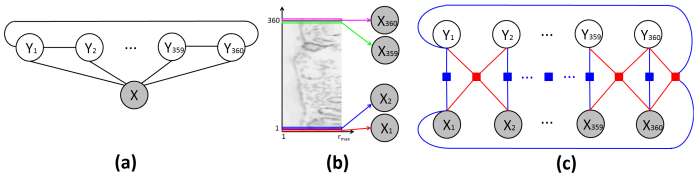

Figure 3: (a) The graphical model of our CRF model; (b) Each row of the polar image is assigned a random variable; (c) The factor graph of our CRF model.

This graph structure is a loop structure only if it contains one more edge which links Y_1 and Y_{360}, otherwise it will be a chain. To avoid the influence of this extra edge, we use two chain structures to approximate this circulate graph, thus enabling efficient inference. This is shown in Fig.4.

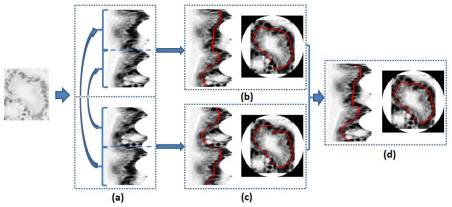

Figure 4: An Efficient Inference Strategy. (a) An image is transformed into two polar images, one's θ ranges from 0 to 2π, and the other's ranges from π to 3π. The Viterbi inference algorithm is performed separately on these two polar images, and the results are shown in (b) and (c). These two results are then combined to generate the final result shown in (d).

We treat the above random field model as a gland proposal module, and then develop another visual feature based support vector regressor (SVR) to verify if the inferred contour corresponds to a true gland. Finally, we combine [1] the outputs of the random field and the regressor to form the GlandVision algorithm for the detection of glandular structures. The flowchart of our complete GlandVision algorithm is depicted in Fig.5.

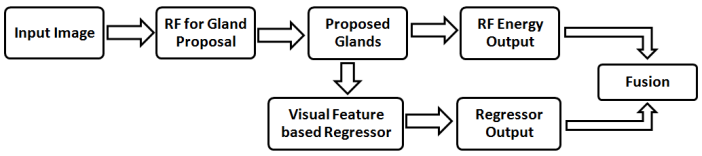

Figure 5: A Complete GlandVision Procedure

Experiments on a dataset of 20 high resolution microscopic images containing 1072 glands have shown the effectiveness of our approach.

[1] Hao Fu, Guoping Qiu, and Hangen He. Feature Combination beyond Basic Arithmetics. In *British Machine Vision Conference(BMVC)*. BMVA, 2011.

[2] John Lafferty, Andrew Mccallum, and Fernando Pereira. Conditional Random Fields : Probabilistic Models for Segmenting and Labeling Sequence Data. In *ICML*, 2001.