KL Divergence based Agglomerative Clustering for Automated Vitiligo Grading

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Vitiligo is the most common depigmenting disorder affecting $0.5-1\%$ of the worldwide population causing disfigurement and seriously lowers quality of life. Vitiligo suffers from a lack of consensus on methods of assessment, which makes it difficult to analyse or compare the outcomes of different studies. Recently, the Vitiligo Area Scoring Index (VASI) [1] and the Vitiligo European Task Force (VETF) [2] tools were proposed to offer more accurate measures of disease severity indexes and treatment evaluation criteria compared to simple clinical photography. Objective methods to measure the spread (area) have been reported by Van Geel et al [4], but a detailed look at multiple regions of depigmentation, especially for darker skin tones (type IV and V) has largely remained an open challenge for the research community. Fig. 1 shows a typical patient with both partial as well as completely depigmented regions.

We propose an automated vitiligo segmentation algorithm with the goal of finding both the completely depigmented as well as the unstable partially depigmented regions within acceptable inter-operator bounds. Our proposed framework can be divided into two conceptual parts. 1) Hierarchical agglomerative clustering of candidate regions (bottom up), 2) probabilistic hypothesis generation for label merging (top down). The comparisons presented in the paper are with respect to the 1st part only. The second part remains common across the algorithms.

We propose symmetric Kullback-Leibler (KL) divergence (Eq. 1) between the two normally distributed clusters, as the preferred distance metric.

$$KL_{C_i,C_j} = \frac{1}{2}(tr(\Sigma_j^{-1}\Sigma_i) + (\mu_j-\mu_i)^T\Sigma_j^{-1}(\mu_j-\mu_i) - d - \ln\frac{|\Sigma_i|}{|\Sigma_j|})$$
$$D_{SKL}(C_i,C_j) = KL_{C_i,C_j} + KL_{C_j,C_i} \quad (1)$$

where C_i and C_j denote the clusters, (μ,Σ) denote the feature mean and covariance, and d is the feature dimension. The log term and the inverse covariance term are obvious bottlenecks in the formulation, which have kept researchers away from using KL divergence based cost functions. In the scenarios, where, the covariances are uniformly kept away from becoming singular, KL divergence turns out to be extremely useful divergence metric. For skin imaging with patch based processes, the covariances over the features seldom go to zero empirically.

Recently, Telgarsky and Dasgupta [3] have proposed agglomerative clustering with Bregman divergences. The generic merge cost for the exponential family is defined as

Definition 1 *[3] Let a proper convex relatively differentiable F and two finite clusters C_1, C_2 be given. Then*

$$\triangle_{F,\theta}(C_1,C_2) = \sum_{i\in\{1,2\}} w_i B_F(\theta_{C_i}, \theta_{C_1\cup C_2}) \quad (2)$$

where $w_i = |C_i|/(|C_1|+|C_2|)$ for $i \in [1,2]$ and $|.|$ denotes the size of the cluster.

where $B_F(\theta_r,\theta_q)$ is the Bregman divergence. Their proposed agglomerative clustering method iteratively selects the pair C_i, C_j which minimizes the merge cost in Eq. 2 and replaces the cluster with $C_i \cup C_j$ [3]. We claim that the symmetric KL divergence in Eq. 1 is an upper bound for the merge cost in Eq. 2 and hence minimizing the symmetric KL divergence leads to a valid clustering algorithm.

Theorem 1 $D_{SKL}(C_1,C_2) \geq \triangle_{F,\theta}(C_1,C_2)$

Algorithm 1 Algorithm outline for vitiligo image segmentation by KL divergence based hierarchical clustering

Require RGB color image, number of final clusters c_F
Generate albedo (A) and shading (S) images
Generate super-pixels (clusters)
Generate multi-dimensional feature set
repeat
  Generate adjacency matrix for the clusters.
  Compute pairwise affinity for neighboring super-pixels (Eq. 1) in the feature space
  Merge the 2 clusters with the lowest affinity and update cluster statistics
until number of clusters $== c_F$
return final clusters

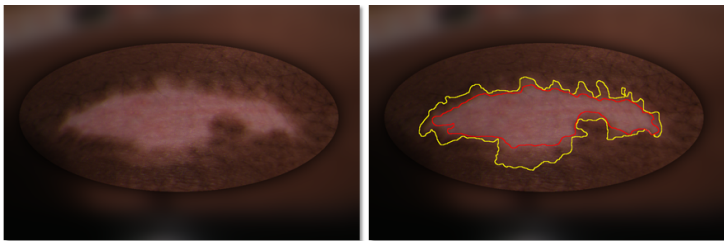

Figure 1: Vitiligo patch and its annotation by an expert. The red boundary marks the completely depigmented skin. The yellow boundary is for the partially depigmented skin. All figures are best viewed in colour.

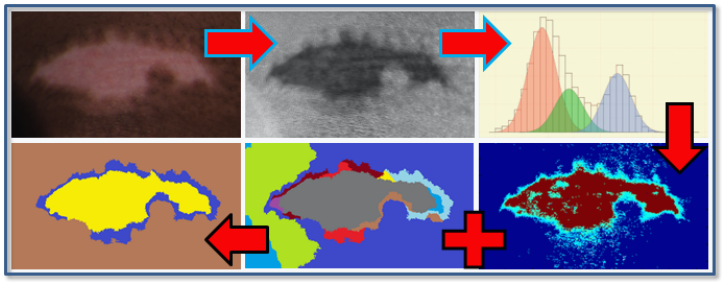

Figure 2: Label hypothesis generation and final labelling. The input image is run through the ICA engine to generate the physiological feature image. The physiological feature is used to learn a Gaussian mixture model. The model is then used to generate a label hypothesis, loosely resembling the ground-truth. The label hypothesis is used in conjunction to the segmentation output to generate the final labels.

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