Semantic Models for Ranking Medical Images using Dirichlet Non-Parametric Mixture Models

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Abstract—With recent advances in diagnostic medical imaging, huge quantities of medical images are produced and stored in digital image repositories. While these repositories are difficult to be analyzed manually by medical experts, they can be evaluated using computerbased methods to enrich the process of decision making. For example, query by image methods can be used by medical experts for differential diagnosis by displaying previously evaluated cases that contain similar visual patterns. Also, less experienced practitioners can benefit from query-by-semantic methods in training processes especially for difficult-to-interpret cases with multiple pathologies. In this article we develop a methodology for ranking medical images based on Dirichlet process nonparametric distributions. Our approach uses natural groupings of images in a generated feature space to evaluate associative semantic mappings. Relevant semantic mappings are then used to generate additive computer models of semantic understanding of visual patterns found in images. We evaluate the performance of our method using mean average precision and precision-recall charts.

Keywords: semantic ranking, HRCT of lung, content based image retrieval, non-parametric modeling, Dirichlet process.

1. INTRODUCTION

Finding patterns of disease in medical images is an important part of radiologists' daily work. Studies show that, in some cases, radiologist performed up to 162 diagnoses per day, three times the reported daily average [1]. For example, radiologists averaged 4.5 minutes for detecting nodules of lung in a HRCT image set by examining in a slice-by-slice mode on average of 100 axial slices [22] with five minutes allocated for writing a report [7]. Such time limitations may affect the diagnosis process by misdiagnoses or missed diagnoses with a potential of impacting patients' health [20]. The most common sources of interpretation errors are related to failure in perception

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and lack of knowledge [22, 26] with significant differences between different levels of expertise [24].

Diagnoses in medical images require extensive knowledge of the semantics of visual patterns, and efficient strategies for analyzing image information. During the decision process, experts use several heuristics previously developed [22] in which tacit knowledge plays a very important role [8]. Tacit or hidden knowledge is especially difficult to communicate during both initial and continuing training and so are likely to be idiosyncratic. For example the visual differences between emphysema and cystic lung can only be observed in the study of walls and regional distribution [29, 31] and can be difficult to differentiate when hard time restrictions affect the decision-making process. With increased amount of medical knowledge and work load, medical experts may face information overload [26] with impact on patients' health due to misdiagnoses or missed diagnoses. Thus image-based diagnosis involves accuracy and efficiency that could be enhanced by technology support. Computer-based methods for clinical support and training can improve the decision making process by the means of differential diagnosis that is provided to the practitioner [14]. The success of such systems depends on the accuracy of visual pattern identification as well as its user-friendliness.

In this article, we propose a methodology of ranking images by content that may be helpful in image-based diagnosis support as well as in training. Our methodology uses non parametric data mining techniques to identify sets of images that are grouped by similarity in a feature space constructed from previously evaluated image cases. We represent each set of images using a parametric Gaussian distribution. Then we evaluate the relevance of these distributions to existent understanding of visual patterns and build knowledge models for domain semantics of interest. These semantic models can be applied to new cases using semantic ranking methods as well as in training using image ranking methods. This paper is organized as follows. Section 2 summarizes the related work in medical image evaluation. Section 3 presents our approach for identifying feature spaces relevant for semantic assignment and introduce semantic modeling in Section 4. We then evaluate the performance of the model in Section 0, and conclude the paper in Section 5.

2. RELATED WORK

Content-based image retrieval (CBIR) methods have significant attention in bio-medical image received databases [1,18,27] because they can augment both clinical, research and educational aspects of biomedicine, while providing a solution to high cost of manual classification and manipulation by medical experts. The success of content based methods is based on the fact that they attempt to construct knowledge models that are similar to experts' knowledge models. Chu et al. [10] developed semantic models using the hierarchical, spatial, temporal, and evolutionary constructs of neural images. The ASSERT system [25] extracts visual patterns related to pathologies of lung found in HRCT images using content-based algorithms and retrieve these findings using a multidimensional hashing index. The approach in IRMA [17] uses six layers of information abstraction from raw feature to knowledge to texture and intensity distribution to classify images by example. The SPIRS system [14] provides content-based methods for retrieval of spine x-rays.

Content-based algorithms use similarities and differences between training instances to create prediction models that can be applied to newly discovered cases [27]. For example, associative learning algorithms [2,3,33], evaluate the continuous feature space to identify subspaces of interest that are discretized and treated as items in a shopping cart for determining associations between feature values and semantics. To address complexity issues, approaches use the support and confidence thresholds to prune the number of candidate association rules. However, this makes these methods susceptible to dependence on the initial conditions [5]. Mixture models have the advantage of reducing overfitting and dependence on initial conditions. Gaussian mixture models were applied to the medical domain. Gaussian mixtures were applied to brain images [15] or breast cancer [30] using the EM algorithm. Although finite mixtures of densities are important in associating feature measurements to semantics spaces, they require assigning prior distributions to all unknown quantities. The Dirichlet process (DP) can be used to model the uncertainty about the functional form of the distribution for parameters in a model since they are generalizations of finite mixture models. In the next sections we will introduce a methodology that uses Dirichlet processes for ranking problems that is applied to HRCT images of lung.

3. FINDING FEATURE REGIONS RELEVANT FOR SEMANTIC ASSIGNMENTS

3.1. Image Collection and feature extraction

The raw information processed by our system is a collection of HRCT images of the lung. To characterize each of these images we apply a suite of computer vision and image processing algorithms that designed to identify visual abnormalities of lung pathologies. Features extracted are texture, shape, and gray scale.

3.2. Gaussian models of semantic assignments

Gaussian models are the most common distributions in data mining that, unlike histograms, provide a parametric, smooth density over a feature space. To compute the relevance of a point *m* in the feature space to a multidimensional Gaussian function $N(\mu, \Sigma)$ with mean vector μ and correlation matrix Σ we use the following the following formula.

$$g(\mathbf{m}|\boldsymbol{\mu},\boldsymbol{\Sigma}) = \frac{1}{(2\pi)^{|\boldsymbol{\mu}|/2}\boldsymbol{\Sigma}^{1/2}} \cdot e^{-1/2(x-\boldsymbol{\mu})^T\boldsymbol{\Sigma}^{-1}(x-\boldsymbol{\mu})}$$
(1)

The proposed semantics query method searches the image databases by visual semantics using the association rules with the form $g(m|\mu, \Sigma) \rightarrow \varsigma$. For a given query, such as "Retrieve images with cysts," the system first evaluates the relevance of images $\iota \in I$ in the image set I to all associations that have as consequent the semantic $\varsigma = "cyst"$. This is accomplished using the features measurements m extracted for the image ι with which we can compute the relevance of the image to the Gaussian $N(\mu, \Sigma)$.

$$T(m_{\iota}|N(\mu, \Sigma)) = \min\left(1, \frac{\tau \cdot g(m_{\iota}|\mu, \Sigma)}{g(\mu|\mu, \Sigma)}\right)$$
(2)

This equation computes the relevance of the measurement *m* to the Gaussian assignment normalized using τ is a weighting factor for support. In our experiments we have used $\tau = 1.25$ that was empirically shown to result in high accuracy. The example in Fig. 1 (a) shows an example of a Gaussian distribution with $\mu = (0.42, 0.4)$ and $\Sigma = (0.05, 0, 0, 0.01)$. The relevance of a point $m_1 = (0.37, 0.41)$ to this function is $T(m_1|N(\mu, \Sigma)) = 100\%$ while the relevance of a point $m_2 = (0.37, 0.87)$ is $T(m_2|N(\mu, \Sigma)) = 36.9\%$

To determine the rank of each image to a semantic ς we define the semantic model $SM_{\varsigma} = \{N(\mu, \Sigma) \rightarrow \varsigma\}$ as a set of all the normal distributions that are relevant to the semantic ς . To compute this relevance, we first sort all $T(m|N(\mu, \Sigma))|N \in SM_{\varsigma}$. Let $rank(T(m|N(\mu, \Sigma)))$ be the rank of the relevance $T(m|N(\mu, \Sigma))$. The final rank

 $T(m|SM_{\varsigma})$ of image ι to semantic ς is given by the following equation:

$$T(m|SM_{\varsigma}) = \sum_{1}^{|SM_{\varsigma}|} \frac{T(m|\mu, \Sigma)}{2^{rank(T(m|\mu, \Sigma))}}$$
(3)

 $T(m|SM_{\varsigma})$ is maximized when the relevance of the image to the most significant normal distribution is higher. The system then ranks images on $T(m|SM_{\varsigma})$ values for the semantic of interest ς and displays them to the users. The image with highest $T(m|SM_{\varsigma})$ is considered the most relevant to the semantics.

3.3. Finding feature regions relevant for semantic assignments

A Dirichlet process $DP(\alpha, G_0)$, with baseline distribution G_0 and scale parameter α , is a distribution over distributions [13]. Let $y_i | i \in [1, N] y_1, \dots, y_n$ be random values drawn independently from some unknown distribution. We can model the distribution of y as a mixture of normal distributions, that contains C mixing components, with the following probability function:

$$P(\mathbf{y}) = \sum_{c=1}^{C} p_c N_c(\mu_c, \Sigma_c)$$
(4)

Assuming that C is finite, we can use a symmetric Dirichlet distribution as prior for pc:

$$P(p_1, \dots, p_C) = \frac{\Gamma(\alpha)}{\Gamma(\alpha/C)^C} \prod_{c=1}^C p_c^{\alpha/C^{-1}}$$
(5)

where $p_c \ge 0 \land \sum_{c=1}^{C} p_c = 1$. The model can be represented according to a Dirichlet process mixture model using the Polya urn scheme [1,19]:

$$y_i | \mu_c, \Sigma_c \sim N(\mu_c, \Sigma_c), i \in [1, N]$$
(6)

$$(\mu_c, \Sigma_c) | G \sim G \tag{7}$$

$$G|\alpha, G_0 \sim DP(\alpha, G_0) \tag{8}$$

In this formula, G is the distribution over (μ_c, Σ_c) that has Dirichlet process prior *DP*. The $(\mu_c, \Sigma_c) | c \in [1, C]$ pairs are sampled from a baseline distribution G_0 and mixed with the positive scale parameter $\alpha | \alpha > 0$. The choice of α is directly proportional with the number of components.

$$\alpha | a_0, b_0 \sim Gamma(a_0, b_0) \tag{9}$$

In this formulas, a_0 and b_0 are parameters that determine the α hyper-parameters parameter of DP. The baseline distribution is the conjugate normal-inverted-Wishart [11]:

$$G_0 = N(\mu | m1, (1/k_0)\Sigma) \cdot IW(\Sigma | \upsilon_1, \psi_1)$$
(10)

Where, k_0 is the scale parameter of the normal part of the baseline distribution, m_1 is the mean of the normal part of the baseline distribution and v_1 and ψ_1 are hyperparameters of the inverted Wishart part of the baseline distribution. These hyper-parameters of G_0 can be computed with the following formulas:

$$m_1 | m_2, s_2 \sim N(m_2, s_2)$$
 (11)

$$k_0 | \tau_1, \tau_2 \sim Gamma(\tau_1/2, \tau_2/2)$$
 (12)



Fig. 1: (a) example of a two-dimensional feature subspace relevant semantic, (b) density of images over a two-dimensional feature space that is used to model semantic assignments

1: GENERATE MODEL(S, F, L) 2: SMS $\leftarrow \{SM_{c}\} \mid \varsigma \in S$ - empty models 3: FOR EACH $f \subset F$ WHERE |f| < maxsize DOCompute Gaussian Distributions C using a 4 : Dirichlet process over f FOR EACH distribution $N(\mu, \Sigma)$ in C DO 5: For each model SM_c i SMS do 6: IF AUC $(SM_c, F, L) \leq AUC (SM_c \cup N(\mu, \Sigma), F, L)$ 7: THEN 8: $SM_{c} \leftarrow SM_{c} \cup \mathbb{N}(\mu, \Sigma)$ FOR EACH $N_i(\mu, \Sigma) \in SM_c$ do 9: IF AUC $(SM_{c}, F, L) \leq AUC(SM_{c} - C)$ 10: N(μ, Σ), F, L) THEN $SM_{\varsigma} \leftarrow SM_{\varsigma} - \mathbb{N}(\mu, \Sigma)$ 11: 12: END IF 13: END FOR 14: END IF 15: END FOR END FOR 16: 17: RETURN SMS 18: END GENERATE MODEL

Fig. 2: Algorithm for creating semantic models SM_{ς} for each semantic $\varsigma \in S$ in the semantic space S. Each semantic model is a set of Gaussian distributions over the feature space F that are relevant to the semantic ς .

$$\psi_1 | v_2, \psi_2 \sim IW(v_2, \psi_2)$$
 (13)

Where, v_2 and ψ_2 are the hyper-parameters of the inverted Wishart prior distribution for the scale matrix ψ_1 , τ_1 and τ_2 are the hyper-parameters for the gamma prior distribution of k_0 , while m_2 and s_2 give the mean and the covariance of the normal prior for the mean m_1 .

The determined Dirichlet process prior can be used to determine conditional distributions of the posterior distribution of model parameters. Posterior sampling is performed using the Markov Chain Monte Carlo Gibbs sampling with auxiliary parameters (Algorithm 8) by Neal [19].

The Dirichlet process returns a number of *C* components which are multivariate Gaussian probability distributions $N(\mu_c, \Sigma_c)$ in which μ_c is a vector representing the mean of the distribution while Σ_c is a covariance matrix. The example Fig. 1 (b) show the image density over a feature space formed by features "FR054" and "FR033". A Dirichlet-process will identify three components on this space.

4. Semantic Modeling

For mapping regions of a feature space *F* into semantics $\varsigma \in S$ from a semantic space *S* we build a semantic model SM_{ς} for each semantic ς . For this we generate candidate feature regions using a Dirichlet process as explained in

Section 3.3 which are used to create additive semantic models as shown in Section 3.2. The pseudo-code for semantic model generation is shown in Fig. 2. The GENERATE MODEL function takes as input the semantic space S, a training feature space F, and label vector for each instance of F. This algorithm examines natural clusters of training instances for subsets $f \subset F$ (line 2 and 3 in the pseudo-code) using a Dirichlet process and generates Gaussian mixtures $N_f(\mu, \Sigma)$. Then, it tests the relevance of each Gaussian distribution in the mixture to each semantic ς using the area-under-curve (AUC) performance measure (see lines 6, 7 in pseudo-code). A Gaussian distribution is added to a semantic model only if it increases AUC. Also, to ensure creating a lessgreedy model, we use the Sequential Forward Floating Selection Algorithm [21] to dynamically perform exclusion of previously selected association rules (see lines 8 to 12 in pseudo code).

Experiments

To evaluate our methodology, we conducted two ranking experiments on the same dataset using two ranking methodologies. Each of these experiments rank images by the following semantics: *Interlobular septal thickening* (SEP), *Bronchiectasis* (BRO), *Tree-in-bud* (TIB), *Small nodules* (SNO), *Ground glass opacity* (GG), *Emphysema* (EMP), *Cysts* (CYS), or *Honecombing* (HON), The first experiment, which we call non-parametric semantic ranking (NPSR) ranks these images using the proposed approach while the second experiment, called associative semantic ranking (ASR) using the method in [1], is used for performance comparison. For both experiments we computed the precision-recall measures.

4.1. Data Source

To evaluate our approach, we used a medical image database, containing 1001 high-HRCT images of lung. For each image, a 128-dimensional feature vector was extracted. Also, these images were labeled by radiologists to include one or multiple labels from the following set: *Interlobular septal thickening* (SEP), *Bronchiectasis* (BRO), *Tree-in-bud* (TIB), *Small nodules* (SNO), *Ground glass opacity* (GG), *Emphysema* (EMP), *Cysts* (CYS), *Honecombing* (HON), *Other* (OTH), or *Healthy* (HLT). Each image tile was assigned a binary degree of relevance to a semantic of 0 (non-relevant) or 1 (relevant). A total of 326 images in this dataset were assigned with multiple labels.

4.2. Results

Fig. 4 shows the precision recall chart for ranking HRCT images of lung using the methodology while Fig. 3 show the precision recall chart for the method introduced in [1]. The NPSR approach returns, on average, a 62.63% mean average precision (MAP) as compared with a 47.53% MAP for the ASR method. The biggest increase in MAP



Fig. 4. Ranking results using the Dirichlet process non-parametric mixture models

was recorded for the *Ground glass opacity*, *Interlobular septal thickening*, and *Honecombing* visual patterns which are difficult to discern for other visual patterns using this feature space. For these visual patterns associative methods would consider some feature regions as irrelevant due to low support or low confidence. The precision recall charts also show an increase in precision especially at high levels of recall. An example for case is for ranking *Cysts* for which the ASR method ranks 88.8% of the images at the top but fails to rank the remainder of 11.2% sue to support limitations. The only visual pattern for which the ASR method returns better AMAP is *Emphysema* for which due to the fact that this visual pattern is similar to *Cysts* and the non-parametric method tends to group them together.

5. CONCLUSIONS AND FUTURE WORK

In this article, we have described a method for associating image content to domain semantics using Dirichlet non-parametric models. Firstly, we identify a set of candidate regions that can be used for semantic assignment using a Dirichlet process and a parametric Gaussian distribution. Then we create weighted additive models for each semantic of interest. The probability that a newly discovered Gaussian distribution is relevant for a semantic assignment is evaluated probabilistically using the area-under-curve (AUC) measure. In our evaluation, we apply and compare our method on a data set of medical images. Then we discussed the significance of our results using precision-recall plots on a resubstitution experiment.



Fig. 3. Ranking results using association rule mining as proposed in [1]

Our evaluation concludes that using non-parametric models for semantic assignments achieve better ranking performance then associative methods. This is due to the fact that associative methods artificially split the space

In this experiment, we chose to use a Gaussian distribution to model the semantic assignment because of its properties. Our experiments show that there is evidence of relevance of non-parametric processes in ranking problems. In our future work we will evaluate other distributions such as asymmetric Gaussian and Sigmoid distributions. We would also like to extend our approach to other medical modalities as well as evaluate the impact of training and semantic space size to evaluate their impact on model creation performance.

6. References

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