Big data in Neurosurgery: Intelligent Support for Brain Tumor Consilium

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Abstract: A brain tumor occurs when abnormal cells form within the brain. Medical imaging plays a central role in the diagnosis of brain tumors. When a brain tumor is diagnosed, a medical team will be formed (consilium) to assess the treatment options presented by the leading surgeon to the patient and his/her family. Using historical evidence-based healthcare data and information directly extracted from images to categorize them may support to increase decision for treatment of patient with brain tumor. Due to its complexity, cancer care is increasingly being dependent on multidisciplinary tumor consilium. That is why it is very important to avoid emotional and quick decisions done by members of consilium. Few studies have investigated how best to organize and run consilium in order to facilitates important decision about patient therapy. We developed and evaluated a multiparametric approach designed to improve the consilium ability to reach treatment decisions. In particular the use of discriminative classification methods such as support vector machines and the use of local brain image meta-data were empirically shown to be important building blocks as support for therapy assign. For efficient classification we used fast SVM classifier with new kernel method.

1 INTRODUCTION

Brain tumors have mainly two types. First is benign tumors are unable of spreading beyond the brain itself. Benign tumors in the brain generally do not essential to be treated and their progress is self-limited. Sometimes they can cause complications because of their position and surgery or radiation can be helpful. And second is malignant tumors are typically called brain cancer. These tumors can extent outside of the brain. Malignant tumors of the brain will always change into a problem if left untreated and a violent approach is almost always warranted. Brain malignancies can be divided into two categories. Primary brain cancer originates in the brain. Secondary or metastatic brain cancer extents to the brain from another site in the body. Cancer arises when cells in the body (in this case brain cells) divide without control. Generally, cells divide in a structured manner. If cells keep separating uncontrollably when new cells are not needed, a mass of tissue forms, called a progress or tumor. The term cancer generally refers to malignant tumors, which can attack nearby tissues and can extent to other parts of the body. A benign tumor does not extent. Last year, an estimated 22,850 adults (12,900 men and 9,950 women) in the United States will be diagnosed with primary cancerous tumors of the brain and spinal cord. It is estimated that 15,320 adults (8,940 men and 6,380 women) will die from this disease this year. About 4,300 children and teens has been diagnosed with a brain or central nervous system in last year. More than half of these are in children younger than 15 (Cancer.net, 2015).

Thanks to the rapid development of modern medical devices and the use of digital systems, more and more medical images are being generated. This has lead to an increase in the demand for automatic methods to index, compare, analyse and annotate them. Care for brain tumors is increasingly complex and often requires specialized expertise from multiple disciplines. Brain tumor consilium reviews provide a multidisciplinary approach to treatment planning that involves doctors from different specialties reviewing

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and discussing the medical condition and treatment of patients (National Cancer Institute, 2012).

In large university hospitals, several terabytes of new data need to be managed every year. Typically, the databases are accessible only by alphanumeric description and textual meta information through the standard Picture Archiving and Communication System (PACS). Data mining can be defined as the process of finding previously unknown patterns and trends in existing tumor images and using that information to build predictive models for consilium decision support (Kincade, 1998).

Alternatively, it can be defined as the process of data selection and exploration and building models using vast data stores to uncover previously unknown patterns (Milley, 2000).

The underlying Digital Imaging and Communication in Medicine (DICOM) protocol supports only queries based on textual content and limited number of parameters present on the DICOM file and defined by the modality (DICOM, 2011). DICOM files contain their modality as part of the meta-data. We suggest to use that information, feature extraction mechanism can take context into account into the feature extraction and decision support process.

The purpose of our study is to automate extraction of DICOM Metadata from the PACS over patients population for specific brain tumor and support brain tumor consilium in making decision for applied therapy. An Support Vector Machine (SVM) classification technique is proposed to recognize in reasonable malignant and benign MRI brain image from historical database in PACS.

2 METHOD

The first step is to automatically extract dicom images semantic and similarity information and expose that information to a classifier in a very efficient way.

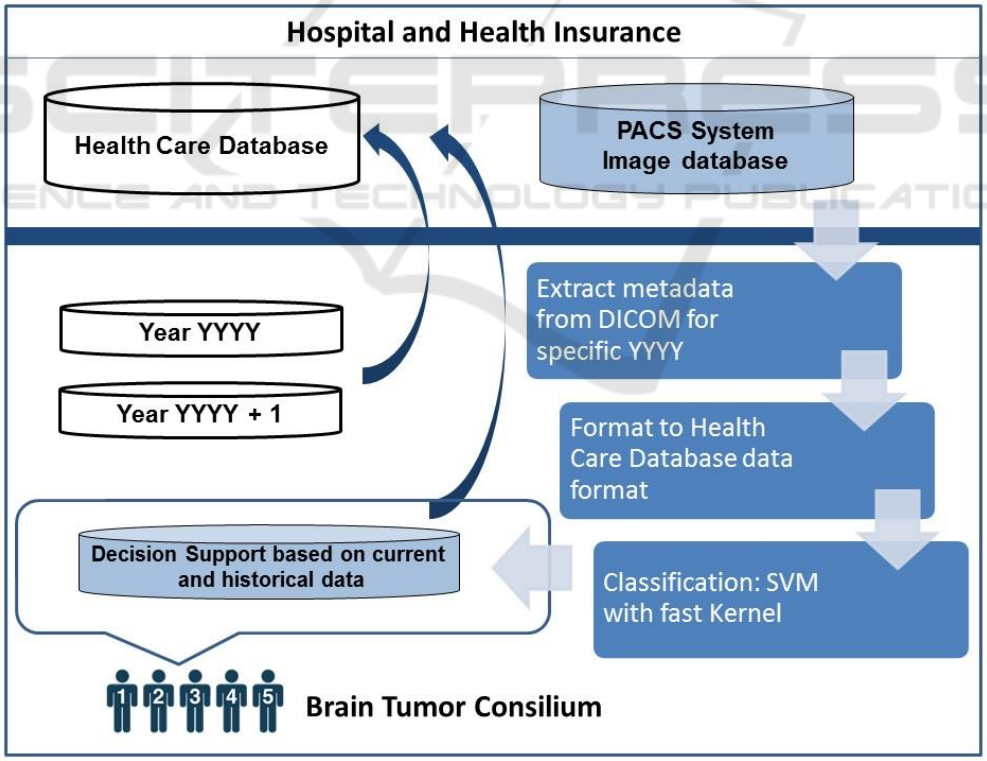


Figure 1. Decision support system for brain tumor consilium. Metadata information from large population of dicom images is analysed by SVM.

The most direct approach to get decision based on images is to match image volume features directly. In this context, content means some property extracted from the image such as color and intensity distribution, texture, shape, or high level features such as the presence of nodes or objects of interest. This approach however is generally not feasible as it may not be clear which volume from one dicom image correspond to which volume in the other image. DICOM objects consist of sets of attribute-value pairs that allow nesting (the values can be other DICOM objects). There are several thousand official attributes, an extension mechanism for private attributes and 27 data types called value representations (VR) for the values (DICOM Part 5, 2011). The data type for each official at tribute is fixed.

Official attributes are identified by a group and element number (16bit unsigned integers usually in hexadecimal notation). Attributes can also represent some kind of real world entity that is only implicitly defined by DICOM or some kind of abstract entity created by the particular hospital. There are important metadata such as pixel parameters, acquisition index, patient dose and geometric information that are generated by the modality and transferred to the PACS database as DICOM metadata.

We have divided metadata into feature sets. General dicom image features, which can be extracted from PACS and can therefore be applied to queries over brain tumor category, and modality specific features. Our concept relies on the automatic extraction of attributes from a dicom image to provide the multiparameters for classifier (Fig. 1).

2.1 Classification

An Support Vector Machine classification technique is proposed to recognize malignant and benign tumors from MRI brain images (meta-data).

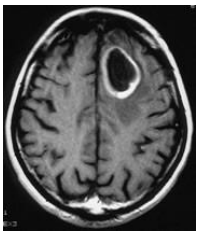
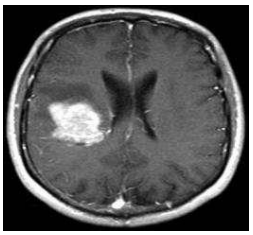
a)  b) 

Figure 2: DICOM images of a a) benign and b) malignant brain tumor.

Benign tumors have well defined edges and are more easily removed surgically. Malignant tumors have an irregular border that invades normal tissue with finger-like projections making surgical removal more difficult. Image source: a) http://neurosurgery.ufl.edu and b) http://cdn.phys.org

2.2 Fast SVM

SVM is one of the successful approaches to multiparametric data analysis. In supervised classification we have a set of data samples (each consisting of measurements on a set of variables) with associated labels, the class types (malignant, benign). These are used as exemplars in the classifier design. The classification experiments in dicom analysis were carried out with a support vector machine (SVM) (Vapnik, 1995).

Discriminative approaches to recognition problems often depend on comparing distributions of features, e.g. a kernelized SVM, where the kernel measures the similarity between histograms describing the features. In many practical cases where performance of classification is significant SVM with standard kernel function like Gaussian Kernel (GK) or Radial Basis Function (RBF) are not suitable.

Recently, the use of kernels in learning systems has received considerable attention. The main reason is that kernels allow mapping the data into a high dimensional feature space in order to increase the computational power of linear machines (see for example Vapnik, 1995, 1998, Cristianini and Shawe-Taylor, 2000).

SVM can be optimized for performance via the kernel methods adapted for dicom image datasets. In Kernel methods, the original observations are effectively mapped into a higher dimensional non-linear space. For a given nonlinear mapping, the input data space X can be mapped into the feature space H:

$$\phi : X \to H \ \ where\ x \to x : \phi(x). \qquad (1)$$

Linear classification in this non-linear space is then equivalent to non-linear classification in the original space. Require Fisher LDA can be rewritten in terms of dot product.

$$K(x_i, x_j) = \phi(x_i) \bullet \phi(x_j) \qquad (2)$$

Unlike Support Vector Machine (SVM) it doesn't seem the dual problem reveal the kernelized problem

naturally. But inspired by the SVM case we make the following key assumption,

$$w = \sum_i \alpha_i \phi(x_i) \tag{3}$$

In terms of new vektor the objective J (α) becomes,

$$\arg\max_{\alpha \in R^n} J(\alpha) = \frac{\alpha^T S_B^\phi \alpha}{\alpha^T S_W^\phi \alpha} \tag{4}$$

Table 1: Most popular kernels used for SVM classification.

Kernels	Formula
Linear	K(x, x')= x. x'
Sigmoid	K(x, x') = tanh(a x. x'+b)
Polynomial	K(x, x') = (1+ x. x')^d
RBF	K(x, x') = exp(- γ || x - x'||^2)
Gaussian	K(x, x') = exp(- γ || x - x'||)

Table 1 present most popular kernel methods. Correspondingly, a pattern in the original input space R^n is mapped into a potentially much higher dimensional feature vector in the feature space H.

The scatter matrices in kernel space can expressed in terms of the kernel only as follows:

$$S_{\mathbf{B}}^\phi = [K_1 K_1^T - KK^T] + [K_2 K_2^T - KK^T] \tag{5}$$

$$S_W^\phi = K^2 - (N_1 K_1 K_1^T + N_2 K_2 K_2^T) \tag{6}$$

$$K_1 = \frac{1}{N_1} \sum_{im \in psoitive} K_{im}$$

$$K_2 = \frac{1}{N_2} \sum_{i,m \in negative} K_{im} \tag{7}$$

$$K = \frac{1}{N} \sum_{i,j \in N} K_{ij} \tag{8}$$

Popular choice is the Gaussian kernel

$$K(i,j) = \exp(-\frac{\| i - j \|^2}{2\sigma^2}) \tag{9}$$

with a suitable width of kernel and must $\sigma > 0$.

So, we have managed to express the problem in terms of kernels only which is what we were after. Note that since the objective in terms of has exactly the same form as that in terms of w.

In this project the input dicom image is not directly fed into SVM as inputs. Instead, a set of simple features is first extracted from meta-data, and then the features are used as inputs. It will be assumed that each dicom image meta-data set z = {b_1, . . . , b_M} is composed of a set of range-bearing measures b_i = (αi, di) where αi and di are the bearing and range measures, respectively

Each training example for the SVM algorithm is composed by one observation z_i and its classification υ_i. The set of training examples is then given by

$$E = \{(z_i, \upsilon_i) : \upsilon_i \in Y = \{\text{benign, malignant}\}\} \tag{10}$$

where Y is the set of classes. In this paper it is assumed that the classes of the training examples are given in advance (benign, malignant). The objective is to learn a classification system that is able to generalize from these training examples and that can later classify day/night in laboratory environment.

Kernel SVMs have become popular for real-time applications as they enjoy both faster training and classification speeds, with significantly less memory requirements than non-linear kernels due to the compact representation of the decision function (Subhransu et. al, 2008). The crossplane kernel, KH_I (t_a, t_b) = n_i=1 min (t_a(i), t_b(i)) is often used as a measurement of similarity between histograms ta and t_b, and because it is positive definite (Odone et.al, 2005) it can be used as a kernel for discriminative classification using SVMs. Recently, crossplane kernel SVMs (call CPSVMs), have been shown to be successful for detection and recognition (Grauman and Darrell, 2005 and 18. Lazebnik et.al, 2006). We based on kernel Intersection Kernel (Subhransu et. al, 2008). Given feature vectors (parameters from DICOM meta-data) of dimension n and learned support vector classifier consisting of m support vectors, the time complexity for classification and space complexity for storing the support vectors of a standard CPSVM classifier is T (p u).

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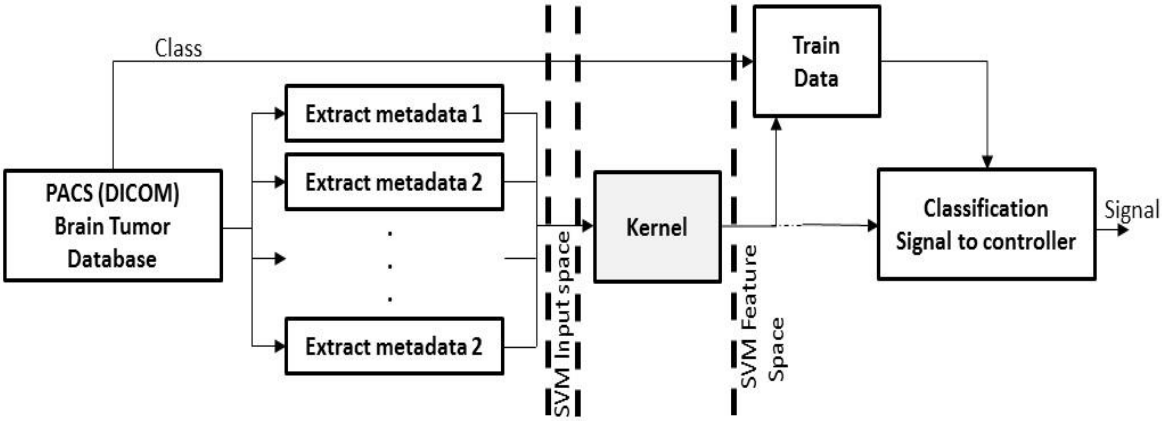

Figure 3: Classification model.

We apply an algorithm for CPSVM classification with time complexity T (u log p) and space complexity T(pu). We then use an approximation scheme whose time and space complexity is T (u), independent of the number of support vectors. The key idea is that for a class of kernels including the crossplane kernel, the classifier can be decomposed as a sum of functions, one for each histogram bin, each of which can be efficiently computed. In dicom anaylsus with thousands of support vectors we also observe speedups up to 2000× and 200× respectively, compared to a standard implementation.

Now we show that it is possible to speed up classification for CPSVMs. For feature vectors x, z $\in R_+^n$, the crossplane kernel is:

$$K(x,z): K(x,z) = \sum_{i=1}^{n} \min(x(i), z(i)) \qquad (11)$$

and classification is based on evaluating:

$$(x) = a_0 + \sum_{i=1}^{m} a_l\, y_l K(x, x_l) + b = \sum_{i=1}^{m} a_l\, y_l \left(\sum_{i=1}^{n} min\big(x(i), x_l(i)\big) \right) + b \qquad (12)$$

Thus the complexity of evaluating h(x) in the naive way is O(pu). The trick for crossplane kernels is that we can exchange the summations in equation 12 to obtain:

$$h(x) = a_0 + \sum_{l=1}^{m} \alpha_l y_l K(x, x_l) + b = \sum_{i=1}^{m} a_l\, y_l \left(\sum_{i=1}^{n} min\big(x(i), x_l(i)\big) \right) + b = \sum_{i=1}^{m} \left(\sum_{i=1}^{n} a_l y_l min\big(x(i), x_l(i)\big) \right) + b = \sum_{i=1}^{n} h_i\big(x(i)\big) \qquad (13)$$

Rewriting the function h(x) as the sum of the individual functions, hi, one for each dimension, where

$$h_i(s) = \sum_{l=1}^{m} \alpha_l y_l \min(s, x_l(i)) \qquad (14)$$

So far we have gained nothing as the complexity of computing each hi(s) is T(p) with an overall complexity of computing h(x) still T(pu). We now show how to compute each hi in T(logp) time.

Consider the functions hi(s) for a fixed value of i. Let $\bar{x}_l(i)$ denote the sorted values of $x_l(i)$ in increasing order with corresponding α' s and labels as $\bar{\alpha}_l$ and $\bar{y}_l$.

If $s < \bar{x}_1(i)$ then $h_i(s) = 0$,

otherwise let r be the largest integer such that

$$\bar{x}_r(i) \le s.$$

Then we have,

$$h_i(s) = \sum_{l=1}^{m} \bar{\alpha}_l \bar{y}_l \min(s, \bar{x}_l(i)) \quad (15)$$

$$= \sum_{1 \le l \le r} \bar{\alpha}_l \bar{y}_l \bar{x}_l(\mathrm{i}) + \mathrm{s} \sum_{r \le l \le m} \bar{\alpha}_l \bar{y}_l$$

$$= A_i(r) + sB_i(r)$$

Where we have defined,

$$A_i(r) = \sum_{1 \le l \le r} \bar{\alpha}_l \bar{y}_l \bar{x}_l(\mathrm{i}), \quad (16)$$

$$B_i(r) = \sum_{r \le l \le m} \bar{\alpha}_l \bar{y}_l \quad (17)$$

Equation 17 shows that hi is piecewise linear. Furthermore hi is continuous because:

$$h_i(\bar{x}_{r+1}) = A_i(r) + \bar{x}_{r+1} B_i(r) = A_i(r+1) + \bar{x}_{r+1} B_i(r+1). \quad (18)$$

Notice that the functions A_i and B_i are independent of the input data and depend only on the support vectors and α. Thus, if we precompute $h_i(\bar{x}_r)$ then $h_i(s)$ can be computed by first finding r, the position of $s = \bar{x}_l$ in the sorted list $\bar{x}$ (i) using binary search and linearly interpolating between $h_i(\bar{x}_r)$ and $h_i(\bar{x}_r+1)$. This requires storing the $\bar{x}_l$ as well as the $h_i(\bar{x}_l)$ or twice the storage of the standard implementation. Thus the runtime complexity of computing h(x) is T(u logp) as opposed to T(pu), a speed up of T(u/logp). In our experiments we typically have SVMs with a few thousand support vectors and the resulting speedup is quite significant.

3 RESULTS

In order to show the validity and classification accuracy of our algorithm we performed a series of tests on few dicom benchmark data sets. Data sets are presented in table 2. We tested a proposed extension of Intersection Kernel in experimental datasets from sample collection dicoms. We use the standard SVM algorithm for binary classification described previously. The regularization factor of SVM was fixed to C = 10. In order to see the effect of generalization performance on the size of training data set and model complexity, experiments were carried out by varying the number of training samples (30, 60, 120, 180, 240) according to a 5-fold cross validation evaluation of the generalization error. The data was split into training and test sets and normalized to minimum and maximum feature values (Min-Max) or standard deviation (Std-Dev).

Table 2: DICOM images dataset for astrocytoma brain tumors from demo dataset. Datasets are divided in malignant tumors and benign tumors.

	Total	Training data	Test data
Images	840	420	420
Malignant tumors	260	130	130
Benign tumors	580	290	290

Results for our classifier are presented in table 3.

Table 3. Classification results for two datasets from two patients using two kernel methods with c = 20.

Dataset 1: Malignant tumors

Training set	Kernel RBF	Training Time/ Classification Time	Classification Accuracy	Intersection Kernel	Training Time/ Classification Time	Classification Accuracy
30	C = 20	16 s / 3s	83.6%±6.7	C = 20	11 s /3s	84.7%±1.6
60	C = 20	27 s / 6s	84.2%±2.6	C = 20	12 s / 4s	85.5%±6.7
120	C = 20	35 s / 10s	85.6%±5.5	C = 20	24 s / 10s	86.2%±1.5
180	C = 20	38 s / 18s	87.2%±1.5	C = 20	22 s / 13s	88.3%±4.3
240	C = 20	48 s / 19s	82.4%±3.9	C = 20	33 s / 17s	82.6%±2.5

Dataset 2: Benign tumors

Training set	Kernel RBF	Training Time/ Classification Time	Classification Accuracy	Intersection Kernel	Training Time/ Classification Time	Classification Accuracy
30	C = 20	14 s / 5s	83.6%±6.7	C = 10	12 s /3s	84.4%±2.6
60	C = 20	27 s / 9s	82.3%±2.5	C = 10	16 s / 4s	82.9%±5.5
120	C = 20	32 s / 12s	85.0%±4.4	C = 10	23 s / 11s	87.1%±1.7
180	C = 20	40 s / 15s	83.1%±1.5	C = 10	27 s / 13s	85.2%±3.4
240	C = 20	45 s / 18s	85.5%±2.7	C = 10	35 s / 13s	82.8%±1.6

4 CONCLUSION

The accuracy of the SVM for classifying malignancies was by average 85.4% (28s) and the negative bening tumors predictive value, 83.61% (24s). The SVM proved helpful in the decision based on imaging diagnosis of brain tumor. The classification ability of the SVM with fast Kernel is nearly equal to that of the standard SVM model, but the SVM with fast kernel has a much shorter training and prediction time (1 vs 189 seconds). Given the increasing size and complexity of data sets, the SVM is therefore preferable for computer-aided decision support. Our method has the potential to predict therapy strategy in fast time, saving a significant amount of time to consilium experts, giving them suggestions, enabling them to quickly move from a single observation object image to a set of similar ones, potentially containing historical decisions in therapy. These supporting decisions, when compared to the current patient dicom image, may strengthen the case for the diagnosis or provide the consilium with additional insight.

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