

# Deep Learning for Automated Extraction of Primary Sites from Cancer Pathology Reports

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**Abstract**— Pathology reports are a primary source of information for cancer registries which process high volumes of free-text reports annually. Information extraction and coding is a manual, labor-intensive process. In this study we investigated deep learning and a convolutional neural network (CNN), for extracting ICD-O-3 topographic codes from a corpus of breast and lung cancer pathology reports. We performed two experiments, using a CNN and a more conventional term frequency vector approach, to assess the effects of class prevalence and inter-class transfer learning. The experiments were based on a set of 942 pathology reports with human expert annotations as the gold standard. CNN performance was compared against a more conventional term frequency vector space approach. We observed that the deep learning models consistently outperformed the conventional approaches in the class prevalence experiment, resulting in micro and macro-F score increases of up to 0.132 and 0.226 respectively when class labels were well populated. Specifically, the best performing CNN achieved a micro-F score of 0.722 over 12 ICD-O-3 topography codes. Transfer learning provided a consistent but modest performance boost for the deep learning methods but trends were contingent on CNN method and cancer site. These encouraging results demonstrate the potential of deep learning for automated abstraction of pathology reports.

**Index Terms**—deep learning, convolutional neural network, natural language processing, information extraction, pathology reports, primary cancer site.

## I. INTRODUCTION

Cancer is the second leading cause of death in the United States [1]. Over the course of a cancer patient's diagnosis and treatment, pathologists record highly descriptive and specific observations of cells and tissues in pathology reports. Because these individualized yet mass produced clinical reports are encoded in mostly unstructured text, the potential accessibility of vast amounts of data is contingent on the performance of natural language processing (NLP) tools for automated information extraction [2].

Cancer registries process a very high volume of pathology reports, hundreds of thousands in the Surveillance, Epidemiology and End Results (SEER) registries alone, which cover 30% of US population [3]. These reports are highly variable, as they come from hundreds of healthcare providers and laboratories. There are also data quality issues due to human fatigue, differences in interpretation and application of coding rules, etc. Moreover, the clinical details from pathology and other reports that are needed to characterize cancer patient trajectories are increasing as patients live longer and have more complex treatments. At this scale, manual information extraction and coding is expensive to sustain, and registries are unlikely to address issues of volume, variability, and timeliness of reporting without some automation.

Since the registries have access to high volumes of electronic pathology reports and coded variables extracted from those reports, a machine learning approach to feature and classifier development could offer an effective path for registries to implement automation using artificial intelligence for information extraction and coding. For cancer registries, an important piece of information in a pathology report is the corresponding ICD-O-3 topographical code, which describes the specific anatomical site of a tumor's origin [4]. Although multiple sites may be mentioned in a pathology report, for the most part, only one primary site is discussed per report. Extraction and coding of primary sites by ICD-O-3 topographical codes provides a well-documented starting point for exploration of deep learning NLP techniques to support cancer surveillance.

Within the biomedical informatics literature, NLP approaches for information extraction range from strictly defined, manually tuned rule-based systems [5], to generalized and domain-specific systems relying on feature-based machine learning classifiers [6], to recent deep learning approaches for both automated feature development [7] and supervised classifier models [8]. Though these prior techniques have individually demonstrated effective performance within their

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own experiments, a systematic comparison of methods across varying distributions of clinical documents has yet to be studied.

Since 1971, Vector Space Models (VSM) utilizing term and document frequency counts as automatic document feature extractors have been used to retrieve information from a corpus of documents [9, 10]. Recent deep learning applications for NLP have resulted in great progress for both automated feature extraction and classification tasks. Multilayered neural networks extend automated feature extraction techniques beyond document-level representation to a machine learned latent vector space representation for words. These word-level learned features do not need to be task specific, as word training has been performed on unlabeled but vast corpora such as Wikipedia or a national periodical such as the Wall Street Journal [11]. These learned word features are called “word embeddings” and like document VSMs, attempt to capture semantic information via observed similarities in word contexts. This completely automated and generalized approach nonetheless resulted in state-of-the-art performance in NLP benchmark subtasks against even highly engineered task-specific prior techniques [11]. Researchers have investigated techniques for making this feature extraction more task-specific with either word pre-training on a domain specific corpus [7, 12] or by simultaneously learning latent word features alongside a particular class task [11]. Previous deep learning approaches focused on the sequential nature of text data with recurrent networks [22] or encoding documents into individual latent feature vectors [13]. Such approaches focus mainly on documents-wide attributes, such as form and structure. Convolutional neural networks (CNN), initially developed for computer vision [14] and subsequently applied to NLP applications [15], demonstrated superior performance for document-level information extraction and classification utilizing word embeddings [16]. Specifically, the CNN’s convolving filters and max-over time pooling scheme result in a highly effective document feature extraction and selection [16], which greatly improve upon the traditional VSM’s limitations of a sparse high dimensionality feature space and inability to directly utilize word order.

In this paper, we investigate the performance of these recent deep learning NLP techniques for extracting ICDs-O-3 codes by conducting two experiments. First, we examine the effect of dataset size and class imbalance on classifier performance. Therefore, our first experiment uses a dataset with only well-populated classes and an expanded dataset including both well and minimally populated classes. In the second experiment, we explore the learning tradeoffs of increased data specificity versus increased data size. We partition our data by primary organ site and evaluate classifier performance against classifiers trained across primary sites.

The manuscript is organized as follows: Section II discusses our dataset used in the information extraction task and describes our model and our experimental procedure in detail. Section III presents our experimental results which we discuss in Section IV.

TABLE I  
ICD-O-3 TOPOGRAPHICAL CODES

Code	Count	Description
C34.0	26	Main Bronchus
C34.1	139	Upper lobe, lung
C34.2	11	Middle lobe, lung
C34.3	78	Lower lobe, lung
C34.9	191	Lung, NOS
C50.1	13	Central portion of breast
C50.2	36	Upper-inner quadrant of breast
C50.3	10	Lower-inner quadrant of breast
C50.4	63	Upper-outer quadrant of breast
C50.5	21	Lower-outer quadrant of breast
C50.8	62	Overlapping lesion of breast
C50.9	292	Breast NOS

TABLE II  
PATHOLOGY REPORT ORIGIN REPOSITORY

Repository	Breast (C50)	Lung (C34)
HI	109	102
KY	96	105
NM	131	113
CT	44	32
Seattle	117	93

## II. MATERIALS AND METHODS

### A. Pathology Dataset

Our analysis used a corpus of 942 de-identified pathology reports matched to 12 ICD-O-3 topography codes corresponding to 7 breast and 5 lung primary sites. For 6 ICD-O-3 codes the dataset included at least 50 observations per code but the remaining 6 ICD-O-3 codes were minimally populated with at least 10 but less than 50 observations per code. Table I describes the 12 topography codes and the corresponding observation count per code included in the database.

The pathology reports were provided from five different SEER cancer registries (CT, HI, KY, NM, Seattle) with the proper IRB-approved protocol. Cancer registry experts manually annotated all pathology reports based on standard guidelines and coding instructions used in cancer surveillance. Their annotations served as the gold standard. For label consistency in our training set, we only used pathology reports with a single topography code sourced only from the “Final Diagnosis” section of the report to minimize variation in our training data, though we investigated further the robustness of our findings when including reports with ground truth labels sourced from other report sections (i.e., e.g. Clinical History, Microscopic Description, Clinical Information). Since some report sections available in each pathology report vary across pathology labs and registries, we aggregated the text content of every section in the pre-processing phase. The average length of the reports was 469 words. Table II includes the number and types of pathology reports provided by each SEER registry.

### B. Vector Space Models and Word-Feature Training

With VSMs, documents within a corpus are encoded with a

feature vector based on word counts, also known as the ‘bag of words’ feature representation [10]. For decades, this conceptually simple and relatively effective document representation was the basis for many NLP tasks, particularly information retrieval and extraction [8, 9]. Likewise, word embedding approaches use observed similarities to derive meaning from word occurrence. Unlike VSMs, word embeddings are learned representations of words rather than observed representations of documents, and are trained with temporal context windows utilizing deep learning feature development techniques. The word vector representation is expressed as the following: given a sequence of words  $x_1, x_2, \dots, x_t$ , there are corresponding word vectors  $w_1, w_2, \dots, w_T$  where  $w_i \in \mathbb{R}^k$  [15]. One recent approach to training word vectors is Mikolov’s word2vec skip-gram method, in which vectors are initialized randomly and a corpus’s word vectors values are trained by generating contexts for the corpus words and maximizing the following objective function for a context containing word  $w_i$ :

$$\frac{1}{T} \sum_{t=1}^T \sum_{-c \leq j \leq c, j \neq 0} \log p(w_{t+j}|w_t) \quad (1)$$

where  $c$  is the size of the training context  $w_1, w_2, \dots, w_T$  and  $p$  is the hierarchical softmax function [17]. In essence, word vectors are trained to predict the text context in which they are likely to appear. In practice, word embeddings are trained by stochastically traversing a corpora’s contexts, building an embedding matrix  $W \in \mathbb{R}^{v \times k}$ , where  $k$  is the pre-specified dimensionality for the vector space for learning embeddings, and  $v$  being the number of learned vectors, effectively corresponding to a vocabulary size.

Since trained word vectors trained to represent a word’s locality within a corpus, training word vectors with a different corpus can capture varying word meanings. Using a more domain specific corpus has been observed to result in improved performance across various biomedical information extraction tasks [7]. Therefore, in our experiments, we compared the performance of a deep learning document classifier using word2vec skip-gram learned embeddings from i) a general purpose corpus, trained with articles collected by Google News, ii) a domain specific corpus in the form of word embeddings trained with biomedical publications hosted on PubMed, as well as iii) untrained randomly initialized embeddings. Using only randomly initialized embeddings, is effectively equivalent to performing word feature learning on the available corpus of clinical documents. We used Kim’s [16] word vector space of 300 and trained the PubMed embeddings using the Gensim python package [18] but imported pre-trained Google News embeddings.

### 1) Preprocessing

After extracting the pathology report text content, we tokenized each document by removing all non-alphanumeric symbols and setting all alphabetical characters to lowercase. Though non-alphanumeric characters can hold semantic meaning, in our dataset these symbols are often ambiguous, such as a period appearing in both end of a sentence and in a decimal number. For the two pre-trained word embeddings, tokenized words were matched with their pre-trained

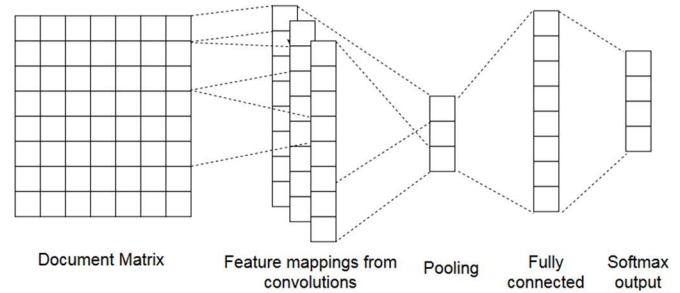


Fig. 1. Convolutional Neural Network Architecture

embedding’s word vector index; if no embedding existed in the embeddings vocabulary but the word’s pathology report document frequency was at least 2, a new word embedding vector would be initialized, otherwise the word would be mapped to an embedding vector corresponding to all words lacking a unique mapping. The decision to remove all non-alphanumeric characters as well as the minimum document frequency was made after considering the size and text content of our dataset and was informed with experimental evidence, though we found these preprocessing decisions did not have a statistically significant effect on performance. As our network is trained, these embedding vectors can be updated via back-propagated errors, thus making these latent features more task-specific. A pathology report with  $n$  words corresponding to word vectors  $w_i \in \mathbb{R}^k$  can be represented by a document matrix

$A \in \mathbb{R}^{n \times k}$ . To accommodate for documents of multiple lengths in our network, we specify a document length parameter  $n$  so that all documents longer than  $n$  will be truncated and documents shorter than  $n$  will be padded with corresponding tokens [15, 16].

### 2) Network Architecture

In machine learning, a convolution is an automatic feature generation technique which processes an input with a trainable regional filter. Similar to applications for image processing, we can apply a convolutional filter to the document matrix with a linear filter with region size  $h$  that corresponds to a context length of  $h$  word vectors. Specifically, we can parameterize a linear filter as a weight matrix  $w$  with dimensions  $h \times k$ . A context window for matrix  $A$  starting from the  $i$ th word vector of  $A$  with length  $h$  can be represented by submatrix  $A[i:i+h-1]$  [15]. A single convolution on the document’s  $i$ th word with context length  $h$  can be denoted as  $o_i = w \cdot A[i:i+h-1]$  where  $o_i \in \mathbb{R}^{n-h}$ . Finally, we apply an activation function  $f$  with a bias term  $b \in \mathbb{R}$  to  $o_i$ , inducing a single feature map  $c_i = f(o_i + b)$ . The final output of a convolutional filter over document matrix  $A$  can be expressed as feature mapping  $c = \{c_1, c_2, \dots, c_n\}$ , which is a representation of every context window of length  $h$  over document matrix  $A$  [15, 16].

Through the extraction of all contexts of a particular length, our CNN learns to consider contexts of multiple sizes simultaneously when classifying a pathology report, producing a “feature mapping” to represent each context size. The subsequent pooling layer trains the convolutional filter to extract a single feature map scalar from each mapping, aggregating the selected contexts by concatenation. This pooling is a highly efficient form of feature selection which

allows our model to classify documents by learning for every convolutional filter which is the most useful context instead of learning some direct document abstraction which can be difficult to fully develop with datasets of our scale [16]. The pooled features connect to a fully connected hidden layer, where we aggregate the selected separate convolutional features and implement our regularization, including dropout. Our final layer is the soft-max (multinomial logistic regression) classifier itself. Further regularization was employed on the hidden layer with an  $l_2$ -normalization of weight vectors. Our network weights were trained with the Adadelta adaptive gradient descent algorithm [16].

### 3) Hyper parameter tuning

For guidance in tuning the model's hyper-parameters, we used Zhang et al's CNN sensitivity analysis [15] as a starting point. Further, we incrementally adjusted model parameters to maximize average class performance (Macro-F). By optimizing for Macro-F, we attempted to optimize for algorithm generalizability across different labels with varying features and numbers of training observations.

To accommodate the wide lengths of pathology reports while maintaining reasonable network train times, we defined the document length input as 1500 words vectors. In our convolutional layer, we used context window sizes of 3, 4 and 5 along with a Rectified Linear Unit activation function. For our pooling strategy, we used max-over time pooling, which selects a single context from the document-spanning convolutions to present to our final soft-max classifier. Finally, to account for class imbalance, we weighed our error costs inversely proportional to a class prevalence in the dataset.

### B. Experimental Design

*Experiment 1 - Class Prevalence:* We first compared performance when the model is developed using data from the well populated classes (6 ICD-O-3 classes with a minimum of 50 pathology reports per class) vs. a model developed using data combining the six well-populated classes with six minimally-populated classes containing 10-49 pathology reports per class.

*Experiment 2: Transfer Learning:* We investigated the cross-label learning capabilities of each model by evaluating classification performance for each primary site (lung, breast) with models trained with only one primary site's data to models trained with the entire dataset.

### C. Comparative Analysis

In our experiments, we compared the proposed word embeddings CNN approach with the baseline NLP approach of unigram and bigram term frequency-inverse document frequency (TF-IDF) vector space model combined with conventional classifiers. This document feature representation is considered a standard approach in both the NLP [10, 19] and the biomedical informatics information extraction literature [20, 21]. Similar to the deep-learning approach, we pre-processed our pathology report data by removing, all non-alphabetical and numeric characters, and stop words. We then tokenized the processed pathology reports into  $n$ -grams of up to length 2 and generated an  $n$ -gram based term-frequency vector

for each report while aggregating a training corpus document-frequency dictionary for each  $n$ -gram. Through model development experimentation, we concluded that utilizing an  $n$ -gram feature space of 400 resulted in optimal performance given our dataset and information extraction task. Therefore, we removed all but the top 400 document-occurring  $n$ -grams from our corpus vocabulary and finalized the pathology report feature vector by dividing each report term frequency vectors by the corpus document frequency vector. We utilized multinomial Naive Bayes (NB), Logistic Regression (LR), and Linear Support Vector Machines (SVM) as our baseline ICD-O-3 topography code classifiers as the literature suggests [19]. To address ICD-O-3 topography code class imbalance, we trained model parameters weighted inversely proportional to an observation's class representation. For network regularization, the optimal dropout rate appeared to be .5, but our  $l_2$  normalization appeared to have little impact on performance metrics.

### D. Performance Evaluation

Each of our two experiments contains two classification tasks; 6-class vs 12-class. We utilize a balanced tenfold cross validation scheme by randomly partitioning the dataset into ten parts with near balanced label distributions. For each fold we use one partition once for testing and combine the rest for our training set, evaluating model performance on the combined predicted-actual results from each fold. We evaluated each model primarily using the standard NLP metrics of micro and macro averaged F-scores, the harmonic mean of related metrics precision and recall. For each ICD-O-3 topography code  $C_j$  from a set of possible code classes in the subtask  $C$ , the number of class true positives is denoted  $TP_j$ , class false positives are  $FP_j$ , and class false negatives are positives  $FN_j$ .

We use class-based metrics precision  $P(C_i)$ , recall  $R(C_i)$ , and F-score  $F(C_i)$  defined as

$$\begin{cases} P(C_i) = \frac{TP_j}{TP_j + FP_j} \\ R(C_i) = \frac{TP_j}{TP_j + FN_j} \\ F(C_i) = \frac{2P(C_i)R(C_i)}{P(C_i) + R(C_i)} \end{cases} \quad (2)$$

Micro-averaged metrics are defined as

$$\begin{cases} p^{micro} = \frac{\sum_{C_j}^c TP_j}{\sum_{C_j}^c (TP_j + FP_j)} \\ R^{micro} = \frac{\sum_{C_j}^c TP_j}{\sum_{C_j}^c (TP_j + FN_j)} \\ F^{micro} = \frac{2p^{micro}R^{micro}}{p^{micro} + R^{micro}} \end{cases} \quad (3)$$

Macro-averaged metrics are defined as

$$\begin{cases} p^{macro} = \frac{1}{|C|} \cdot \sum_{C_j}^c P(C_j) \\ R^{macro} = \frac{1}{|C|} \cdot \sum_{C_j}^c R(C_j) \\ F^{macro} = \frac{1}{|C|} \cdot \sum_{C_j}^c F(C_j) \end{cases} \quad (4)$$

TABLE III  
EXPERIMENT I – CLASS PREVELANCE RESULTS

Minimally Populated – Class Count >10 – 12 ICD-O-3 topography code classes						
Approach	Micro-F	Avg	Macro-F	Avg	Macro-P	Macro-R
TF-IDF	Naïve Bayes (NB)	0.591 (0.561,0.622)	0.222 (0.207,0.239)		0.234 (0.217,0.251)	0.225 (0.207,0.239)
	Logistic Regression (LR)	0.654 (0.627,0.688)	0.263 (0.250,0.281)	0.639	0.278 (0.255,0.294)	0.280 (0.266,0.294)
	Support Vector Machine (SVM)	0.672 (0.639,0.700)	0.291 (0.273,0.303)	0.259	0.291 (0.276,0.300)	0.302 (0.286,0.315)
CNN	Google News pre-trained	0.705 (0.674,0.735)	0.342 (0.324,0.372)		0.353 (0.323,0.372)	0.358 (0.334,0.374)
	PubMed pre-trained	0.713 (0.676,0.737)	<b>0.389</b> (0.338,0.411)	0.713	<b>0.399</b> (0.359,0.421)	<b>0.407</b> (0.360,0.432)
	No pre-training	<b>0.722</b> (0.682,0.740)	0.372 (0.334,0.409)	0.368	0.372 (0.347,0.415)	0.393 (0.359,0.422)
Well Populated – Class Count > 50 - 6 ICD-O-3 topography code classes						
Approach	Micro-F	Avg	Macro-F	Avg	Macro-P	Macro-R
TF-IDF	Naïve Bayes (NB)	0.679 (0.655,0.718)	0.475 (0.452,0.525)		0.500 (0.471,0.523)	0.500 (0.472,0.525)
	Logistic Regression (LR)	0.744 (0.722,0.774)	0.546 (0.539,0.612)	0.728	0.587 (0.540,0.612)	0.552 (0.521,0.570)
	Support Vector Machine (SVM)	0.760 (0.745,0.802)	0.640 (0.600,0.672)	0.554	0.684 (0.633,0.723)	0.625 (0.580,0.651)
CNN	Google News pre-trained	0.794 (0.756,0.815)	0.687 (0.637,0.708)		0.727 (0.671,0.772)	0.692 (0.667,0.738)
	PubMed pre-trained	0.797 (0.761,0.817)	0.688 (0.640,0.712)	0.804	0.733 (0.672,0.779)	0.695 (0.656,0.723)
	No pre-training	<b>0.811</b> (0.762,0.829)	<b>0.701</b> (0.642,0.723)	0.687	<b>0.737</b> (0.679,0.781)	<b>0.707</b> (0.649,0.733)

In summary, micro-averaged metrics have class representation roughly proportional to their test set representation, whereas macro-averaged metrics are averaged by class without weighing by class prevalence [20]. Since micro averaged precision, recall, and F-scores are equivalent for multiclass single-label tasks [24], we will use both the micro and macro F-score metric and only the macro average for the recall and precision metrics.

### III. RESULTS

#### A. Class Prevalence

Table III shows the performance metrics of the first experiment comparing model performance with a minimally-populated 12 class task compared to a well-populated 6 class task. The Table includes 95% confidence intervals for each performance metric, derived using bootstrapping. The proposed CNN classifier consistently performed better than the vector-space models in both the minimally populated classification subtask and the well-populated classification subtask. The TF-IDF approaches averaged micro- and macro-F scores at 0.639 and 0.259 respectively and the CNN approaches averaged micro- and macro-F at 0.713 and 0.368 for the minimally populated task. The TF-IDF approaches averaged micro- and macro-F scores at

0.728 and 0.554 respectively and the CNN approaches averaged micro- and macro-F scores at 0.804 and 0.692 for the well populated task. CNNs consistently outperformed all TF-IDF approaches. Although, the CNN performance metrics were consistently higher than those achieved by SVM, most differences were not statistically significant with the exception of Macro-F.

Figures 2,3,4,5 compare the aggregated normalized confusion matrices for the highest Macro-F scoring model from each approach in the minimally populated classification subtask and the well-populated classification subtask. The true-positive diagonal has been identified with a black line. False-positives are indicated on the vertical axis and false-negatives on the horizontal. From this, we see that the CNN approaches predict fewer false positives for the C34.9 and C50.9 classes, particularly for the breast classes in the well populated task.

#### B. Transfer Learning

Table IV shows the performance metrics of the second experiment comparing separate breast and lung classification performance for primary site models trained on data split by primary site compared to a joint primary site classifier. For the TF-IDF methods, joint training appears to slightly decrease the micro- and macro-F scores. The opposite trend was observed

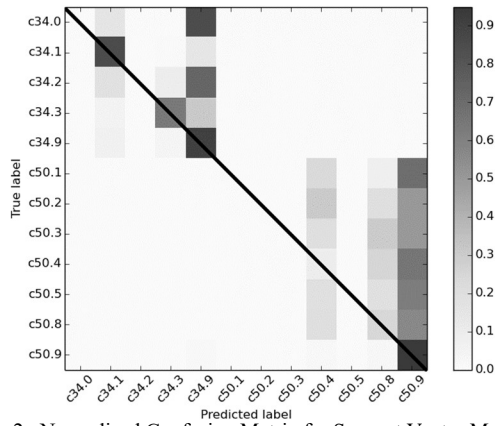


Fig. 2. Normalized Confusion Matrix for Support Vector Machine Minimally Populated Task

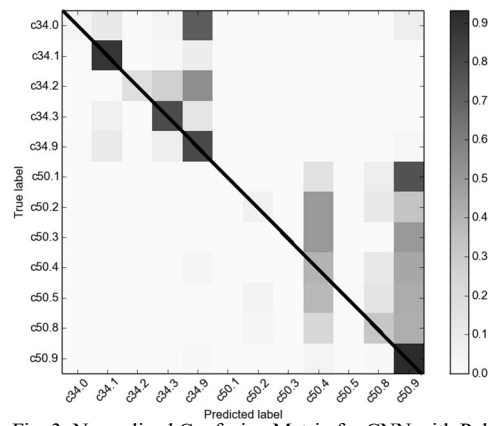


Fig. 3. Normalized Confusion Matrix for CNN with PubMed Word Vectors Minimally Populated Task

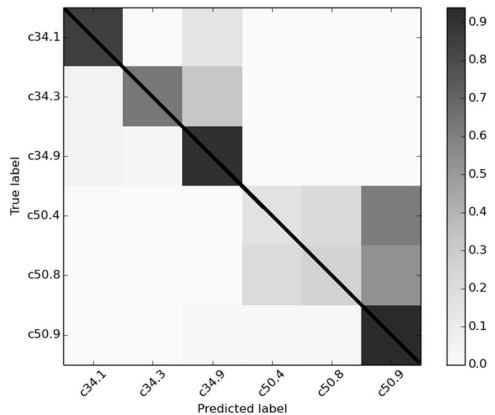


Fig. 4. Normalized Confusion Matrix for Support Vector Machine Well Populated Task

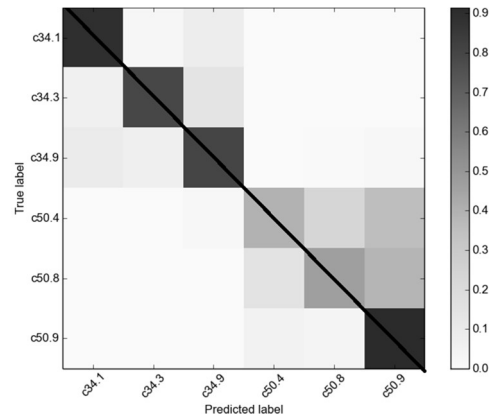


Fig. 5. Normalized Confusion Matrix for CNN with Untrained Word Vectors Well Populated Task

for CNN with joint training resulting in a slight but consistent improvement across embeddings methods and cancer sites. Notable improvement was observed for Breast ICD-O-3 codes; the embeddings without pre-training resulted in substantial performance increases with micro- and macro-F scores of 0.685 and 0.265 respectively compared to 0.631 and 0.193 for split training. For Lung ICD-O-3 codes the PubMed corpus appeared to be superior with joint training resulting in micro- and macro-F scores of 0.782 and 0.606 respectively. and 0.501 and 0.606 for split and joint training respectively. For the breast codes with split training, the Google News embeddings performed best with micro-F scores of 0.644 and macro-F scores of 0.213; the embeddings without pre-training resulted in substantial performance increases in breast class with joint training resulting in micro-F scores of .685 and macro-F scores of 0.265. Overall, this experiment demonstrated the potential benefits of CNN joint training by transferring learning across primary cancer sites although the general trend appeared to be contingent upon the cancer site and the embeddings training method.

#### IV. DISCUSSION

Based on the performance metrics shown in tables III and IV, we see that the word-vector representation with CNN classifier performs consistently better than conventional TF-IDF approaches on every metric, particularly macro-F. It is notable that the most commonly occurring ICD-O-3 topography labels

C50.9 and C34.9 correspond to a breast or lung tumor in location ‘Not Otherwise Specified’. The normalized confusion matrices show how class imbalance and label ambiguity result in frequent false-positives for the TF-IDF feature representation, even for the well populated classes. Although the CNN improvements over macro-F scores resulted from improved performance in classifying well populated codes with less than 50 examples (as illustrated in Figures 2-5), poor performance in classifying rare topographic codes in the minimally populated subtask demonstrates the well-known need for sufficient labeled training data when using deep learning.

In our experiments, we observed that none of the word vector pre-training approaches consistently outperformed the others, though in some specific tasks, one pre-training approach may perform best within that task. For example, compared to the other pre-training approaches, the PubMed embeddings achieved the highest performance metrics for both the joint-trained and split-trained lung classification tasks, but performed second-best in the breast classification task to the Google News embeddings for split training and the no-pretraining, embeddings for joint training. Though other researchers identified performance increases from using domain specific or pre-trained embeddings over randomized embeddings [4, 14]. Our labeled dataset’s comparatively small size, class

TABLE IV  
EXPERIMENT 2 – TRANSFER LEARNING RESULTS

Split Trained – 7 Breast and 5 Lung ICD-O-3 Topography Code Classes									
Approach		Breast Generic Site - 7 ICD-O-3 Classes				Lung Generic Site - 5 ICD-O-3 Classes			
		Micro-F	Macro-F	Macro-P	Macro-R	Micro-F	Macro-F	Macro-P	Macro-R
TF-IDF	NB	0.573	0.182	0.170	0.203	0.638	0.339	0.415	0.357
	LR	0.590	0.143	0.174	0.163	0.737	0.438	0.477	0.443
	SVM	0.618	0.191	0.186	0.204	0.774	<b>0.509</b>	<b>0.500</b>	<b>0.590</b>
CNN	GNews	<b>0.644</b>	<b>0.213</b>	0.218	<b>0.236</b>	0.765	0.473	0.461	0.494
	PubMed	0.631	0.205	<b>0.221</b>	0.226	<b>0.781</b>	0.501	0.488	0.531
	No pre-training	0.631	0.193	0.185	0.217	0.772	0.481	0.475	0.503
Joint Trained – 12 ICD-O-3 Topography Code Classes									
Approach		Breast Generic Site - 7 ICD-O-3 Classes				Lung Generic Site - 5 ICD-O-3 Classes			
		Micro-F	Macro-F	Macro-P	Macro-R	Micro-F	Macro-F	Macro-P	Macro-R
TF-IDF	NB	0.564	0.168	0.162	0.184	0.620	0.301	0.411	0.340
	LR	0.586	0.143	0.161	0.161	0.727	0.440	0.461	0.446
	SVM	0.602	0.168	0.160	0.184	0.751	0.472	0.478	0.479
CNN	GNews	0.643	0.241	<b>0.266</b>	0.255	0.774	0.485	0.476	0.502
	PubMed	0.653	0.234	0.254	0.256	<b>0.782</b>	<b>0.606</b>	<b>0.602</b>	<b>0.619</b>
	No pre-training	<b>0.685</b>	<b>0.265</b>	<b>0.266</b>	<b>0.291</b>	0.764	0.522	0.520	0.535

distribution, or merely the pathology report's unique language style may be the cause. To explore this, we attempted to utilize  $n$ -grams derived from a PubMed corpus as features [23]. All our TF-IDF classifiers performed equally poorly for both classification tasks, with dramatically low micro-F and macro-F scores, indicating an inability for this representation to meaningfully differentiate between our pathology reports (detailed results not shown here due to inferior performance). Finally, although we did not observe consistent performance superiority among the pre-training CNN approaches, we can distinguish word embeddings' ability to transfer information across corpora while maintaining adequate representation of the data.

In our experiments, the various implementation parameters such as the CNN optimal filter window size, the minimum number of word occurrences required for a unique embedding vector, and the exclusion of non-alphanumeric characters were set based literature recommendations that seemed intuitively appropriate for the specific task [15]. For example, despite using entire pathology reports as network inputs, we found the CNN filter window sizes of 3, 4 and 5 used in sentence classification were still effective. This may be task related, as it seems probable that topographical code may be inferred from such a small context. To set the minimum number of word occurrences required for a unique embedding vector, we empirically investigated a range of 1 to 5. We observed that using a minimum document frequency parameter of 2 worked well across all tasks and word embeddings methods, although the differences were not statistically significant. Similarly, with respect to the inclusion or exclusion of non-alphanumeric

characters, there was no statistical significance among the various performance metrics. Previous deep learning NLP experiments using less domain-specific training sets have retained non-alphanumeric characters as individual punctuation tokens with individual embedding vectors [15]. However, we chose to exclude the non-alphanumeric characters since they tend to be ambiguous in pathology reports. Although the above implementation decisions had marginal effects on classifier performance, it remains unclear if our observations are a result of the writing style of the pathology reports, the particular information extraction task, or merely just because of the relatively low number of training observations.

A possible limitation in our study is that our corpus included pathology reports for which the ground truth was sourced only using the final diagnosis section of the report. To better understand the impact of our case selection criterion, we performed a set of additional experiments comparing the performance of our original final-diagnosis-only trained CNNs against networks trained with an additional 144 pathology reports with ICD-O-3 labels sourced from outside the final diagnosis section (e.g., synoptic report, clinical history). The 12-class prevalence was similar to the one in the original dataset. In a series of cross-validation experiments, we observed that the reported trends remained consistent. Although several differences were noted, none of them turn out to be statistically significant. This finding suggests that the CNN approaches are fairly robust.

Although the training data used for these experiments was small relative to the total volume and variety of pathology reports used in state and national cancer surveillance, and the

primary site variable is relatively well-characterized, this work was an important first step in applying deep learning NLP methods to assist the work of cancer registries cancer. Work is underway to obtain a larger set of training and validation data from cancer registries to expand the scale and scope of this approach.

## V. CONCLUSION

We performed a set of experiments comparing the ICD-O-3 topographical information extraction performance of a temporal convolutional network against a more traditional TF-IDF classifier approach over varying datasets of pathology reports. We observed that consistently the CNN outperformed the more traditional classifier, peaking at a micro-F score of 0.811 and a macro-F score of 0.701 for the 6-class task and achieving an overall micro-F score of 0.722 and a macro-F score of 0.389 for the 12-class task. We also tested how pre-trained word embeddings features on differing corpora can influence performance on certain subtasks. Our results suggested that for the information extraction problem with well-populated classes randomized embeddings lead to superior performance. However, when the classification task included classes with low prevalence, pre-trained embeddings achieved better performance.

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