DEPARTMENT OF INFORMATICS
M.Sc. IN COMPUTER SCIENCE

M.Sc. Thesis

"Document Reranking with Deep Learning in Information Retrieval"

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ATHENS, JUNE 2018

Acknowledgements

I would like to thank my supervisor Ion Androutsopoulos for his continuous guidance and support, as well as my second supervisor Ryan McDonald for his valuable help and ideas that formed much of the content of this thesis.

I would also like to thank the members of AUEB's Natural Language Processing group, especially Dimitris Pappas and Polyvios Liosis for the discussions and ideas that we exchanged on our closely related works.

A special thanks goes to Makis Malakasiotis for his help and guidance during my – relevant to this work – B.Sc. thesis and Giannos Koutsikakis for the great cooperation and useful discussions that we had throughout our M.Sc. studies.

Finally, a big thanks goes to my family for their continuous support and patience.

Abstract

In this thesis, we investigate the use of deep artificial neural networks (Deep Learning) for document re-ranking in Information Retrieval (IR). In particular, we explore the DRMM model of Guo et al. (2016) and the PACRR model of Hui et al. (2017) and we propose various improvements. Due to the high complexity of neural networks, we use these models to rerank a list of top N documents returned by a conventional search engine, for a user query. The presented models are tested on data from the BIOASQ challenge (Tsatsaronis et al., 2015) and the TREC ROBUST 2004 ad-hoc retrieval dataset (Voorhees, 2005), showing that they outperform strong traditional IR baselines such as BM25. Moreover, we report the results of our participation in the 6^{th} BIOASQ challenge as Athens University of Economics and Business (AUEB), achieving very competitive results.

Περίληψη

Στην παρούσα διπλωματική εργασία, εξετάζουμε τη χρήση βαθέων τεχνητών νευρωνικών δικτύων (Deep Learning) για την ανακατάταξη εγγράφων σε συστήματα Ανάκτησης Πληροφοριών. Πιο συγκεκριμένα, εξερευνούμε το μοντέλο DRMM (Guo et al., 2016) και το μοντέλο PACRR (Hui et al., 2017) και προτείνουμε βελτιώσεις πάνω σε αυτά. Λόγω της υψηλής πολυπλοκότητας των νευρωνικών δικτύων, χρησιμοποιούμε αυτά τα μοντέλα για να ανακατατάξουμε τα πρώτα N κείμενα που επιστρέφονται από μία συμβατική μηχανή αναζήτησης, δοθέντος ενός ερωτήματος χρήστη. Τα μοντέλα αξιολογούνται σε δεδομένα που προέρχονται από το διαγωνισμό BIOASQ (Tsatsaronis et al., 2015) καθώς και σε δεδομένα από το σύνολο αξιολόγησης TREC ROBUST 2004 (Voorhees, 2005) επιτυγχάνοντας υψηλότερες επιδόσεις από παραδοσιακές μεθόδους κατάταξης κειμένων, όπως το BM25. Επιπλέον παρουσιάζουμε τα αποτελέσματα της συμμετοχής μας στον 6ο διαγωνισμό του BIOASQ ως Οικονομικό Πανεπιστήμιο Αθηνών (ΟΠΑ), στον οποίο επιτύχαμε πολύ ανταγωνιστικά αποτελέσματα.

Contents

Chapter 1

Introduction

1.1 The ad-hoc retrieval task

This thesis examines the use of artificial neural networks for the task of document reranking in an Information Retrieval (IR) and more specifically, ad-hoc retrieval task. In ad-hoc retrieval a query is given as input in natural language form and the system returns a ranked list of documents that should contain enough information to answer the query, or in other words to cover the information need of the query. Documents in this list that do contain information to answer the query are called relevant documents, while the rest are called non-relevant. The higher the position of the relevant documents in the ranked list, the better the performance of the system i.e. the experience of the user submitting the query. An other characteristic of ad-hoc retrieval is that it is based solely on the document's text and no other additional information like user feedback (Joachims, 2002) or citation based characteristics extracted with algorithms like PageRank (Page et al., 1999) and HITS (Kleinberg, 1999), as so happens in standard information retrieval systems like web search engines.

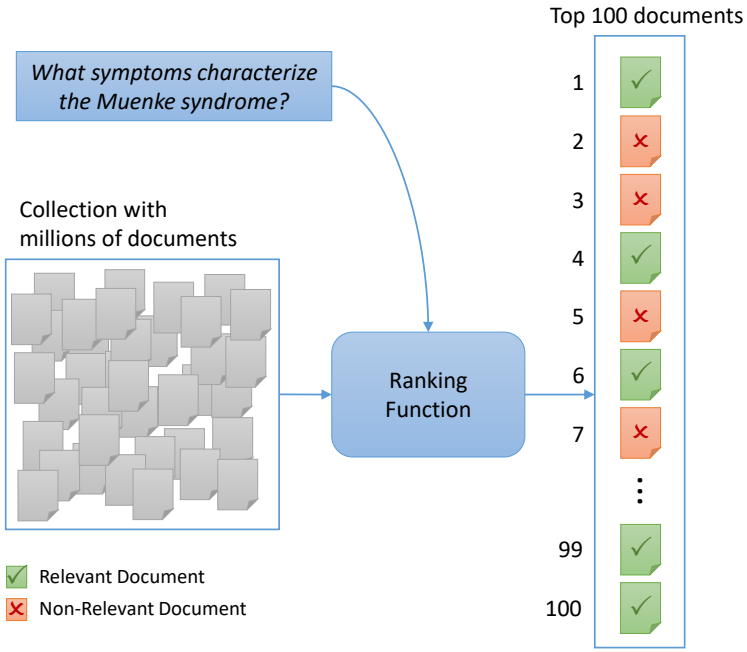


FIGURE 1.1: Standard ad-hoc Retrieval pipeline.

Figure 1.1 shows the standard pipeline of an ad-hoc retrieval system. A large collection is available, usually containing millions of documents. The most important component of the system is the ranking function. Given a query from a user, the ranking function calculates a relevance score between the query and each one of the documents in the collection. Then, documents are sorted by decreasing relevance score and the top N in the list are shown to the user. A typical example of a ranking function is Query Likelihood (QL) which builds a language model for each document in the collection and then scores each document by the probability assigned to the query by the document's language model (Ponte and Croft, 1998). Ranking functions based on Term Frequency (TF) and Inverse Document Frequency (IDF) are also widely used in information retrieval. A TF-IDF based ranking function that has gained popularity in traditional information retrieval is BM25 (Robertson et al., 1995). Among other improvements, it differs from a common TF-IDF model in the fact that it takes into account the document length in order to avoid being affected by highly varied document lengths in a collection.

1.2 The goal of the thesis

The main limitation of traditional information retrieval models like QL and BM25 is that they are based on exact word matching (i.e., common words between a query and a document). Techniques like stemming are used to match words based on the word root, in order to increase word matching, however problems like synonymity are not tackled. Also polysemy can not be detected since these models are not context aware.

In the last few years, multi-dimensional dense word representations (word embeddings) produced by shallow neural networks (Mikolov et al., 2013; Pennington et al., 2014) have gained much popularity and are widely used in various Natural Language Processing (NLP) tasks. Their basic characteristic is that the representations of syntactically or semantically similar words are close to each other in this multi-dimensional space. For example the words *pain* and *ache* have similar dense representations in this model, where these two words would be totally different in a conventional IR system relying on exact term matching. In a previous work we have examined the use of word embeddings for information retrieval in order to utilize their benefits, by using centroids of word embeddings to represent queries and documents and then applying a simple similarity metric on these representations as well as a reranking filter that operates directly on word embeddings (Brokos, Malakasiotis, and Androutsopoulos, 2016). However, traditional IR systems like BM25 seemed to outperform this approach.

In this work we will examine the use of deep neural network architectures that operate on top of the word embeddings of a query and a document and their interactions, as a document ranking function. Deep learning models are computationally expensive, in contrast with a basic requirement of IR systems, which is to respond quickly to a user query (e.g., less than 1 second). Hence, we will use these models to rerank the top N documents returned by a conventional search engine that uses BM25, as illustrated in Figure 1.2 for $N = 100$. A possible limitation of this approach is that the neural document ranking is limited by the performance of the conventional retrieval. However, experimental results show that there is a lot of room

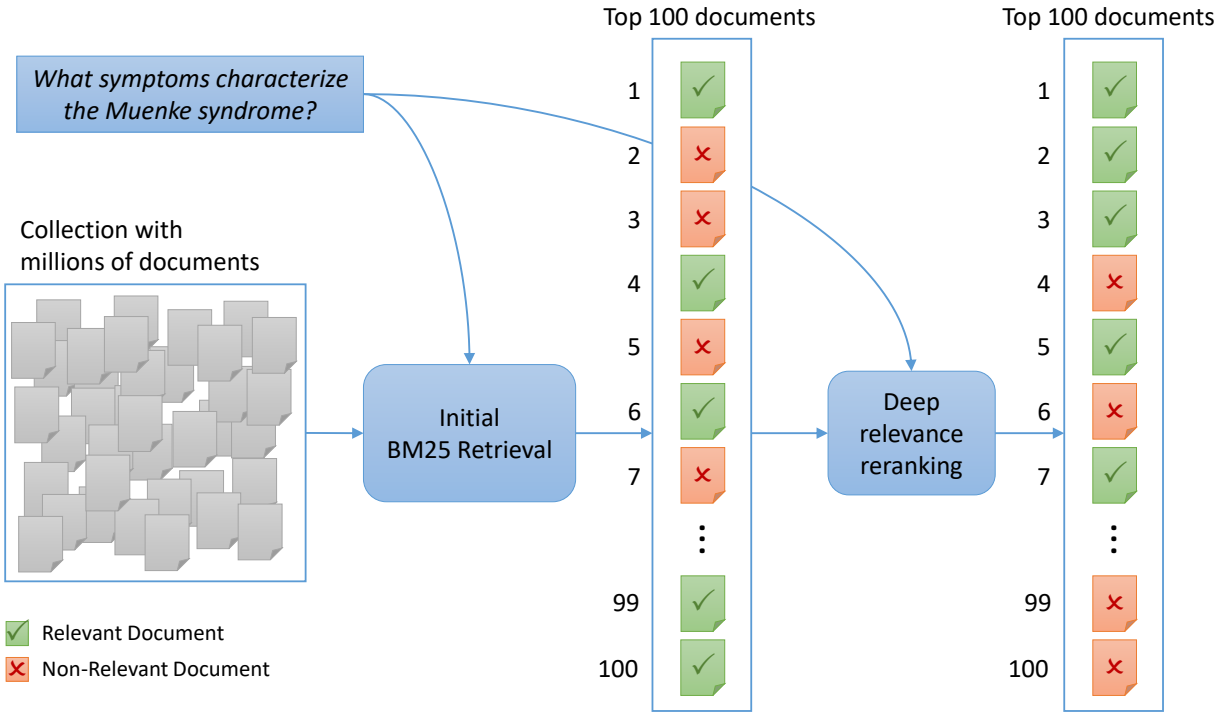


FIGURE 1.2: Ad-hoc retrieval with deep relevance document reranking.

for improvement in the ranking of the list returned by BM25, i.e., there are many relevant documents but in low (bad) positions.

More specifically, we will use and improve two recently proposed document relevance ranking models, the Deep Relevance Matching Model of Guo et al., 2016 and the Position-Aware Convolutional-Recurrent Relevance matching model of Hui et al., 2017 using also improvements proposed by the aforementioned authors (Hui et al., 2018). We test the models on data from the BIOASQ challenge (Tsatsaronis et al., 2015) and the TREC ROBUST 2004 ad-hoc retrieval dataset (Voorhees, 2005). Experimental results show that the proposed models, combined with a set of additional exact term matching features, outperform traditional BM25 based baselines.[1]

Moreover, we report the results of our participation in the document retrieval task of the 6^{th} year of the BIOASQ challenge, using the model that performed best on development data, showing that it achieves competitive results, usually outperformed only by other deep learning methods based or inspired by the presented models, submitted by our team as Athens University of Economics and Business (AUEB).

[1]The code and data used for the experiments of this thesis are available at: https://github.com/gbrokos/document-reranking-with-deep-learning-in-ir

1.3 Outline

The rest of the thesis is organized as follows:

- Chapter 2 - Description of the BM25 retrieval model and the deep learning reranking models.
- Chapter 3 - Description of the datasets used and the experimental setup, along with presentation of the experimental results.
- Chapter 4 - Discussion about recent work related to document ranking.
- Chapter 5 - Discussion about the findings and contributions of the thesis, as well as ideas for future work.

Chapter 2

Methods

This chapter describes methods that can be used to produce a relevance score $rel(Q, D)$ for a document D given a query Q. Starting with the BM25 baseline we move to the deep learning models that will be used to rerank the list of documents retrieved by BM25. Finally, additional features capturing strong exact term matching signals are presented and integrated into the deep learning models.

2.1 The BM25 scoring function

As already mentioned, we will utilize efficient retrieval frameworks (search engines) to reduce the number of documents for the neural network reranking models. BM25 (Robertson et al., 1995) is a scoring function that is widely used in many traditional search engines. Given a query Q containing n terms $q_1, q_2, \ldots, q_n$ and a document D, BM25 calculates a relevance score based on exact matching of word uni-grams between the query and the document as follows:

$$rel(Q, D) = \sum_{i=1}^{n} IDF(q_i) \cdot \frac{TF(q_i, D) \cdot (k_1 + 1)}{TF(q_i, D) + k_1 \cdot (1 - b + b \cdot \frac{|D|}{avgDocLen})} \tag{2.1}$$

where $TF(q_i)$ is the Term Frequency of the i-th query term in document D and $IDF(q_i)$ is the Inverse Document Frequency of term q_i (Eq. 2.2), $|D|$ is the length of document D in tokens and $avgDocLen$ is the average length of the documents in the corpus. Finally k_1 and b are parameters to be tuned.

IDF is computed as follows:

$$IDF(q_i) = \log \frac{|D|}{df(q_i) + 0.5} \tag{2.2}$$

where $df(q_i)$ is the document frequency of the word q_i, $|D|$ is the total number of documents in the corpus and 0.5 is a smoothing factor. As other TF-IDF based methods, BM25 relies on exact term matching between the query and the document. However, BM25 is usually superior to other simpler TF-IDF methods, possibly due to its document length normalization factor.

2.2 Neural network architectures for document relevance ranking

Neural networks for document relevance ranking often belong to one of the following categories: representation-focused and interaction-focused models (Guo et al., 2016; Zhang et al., 2016).

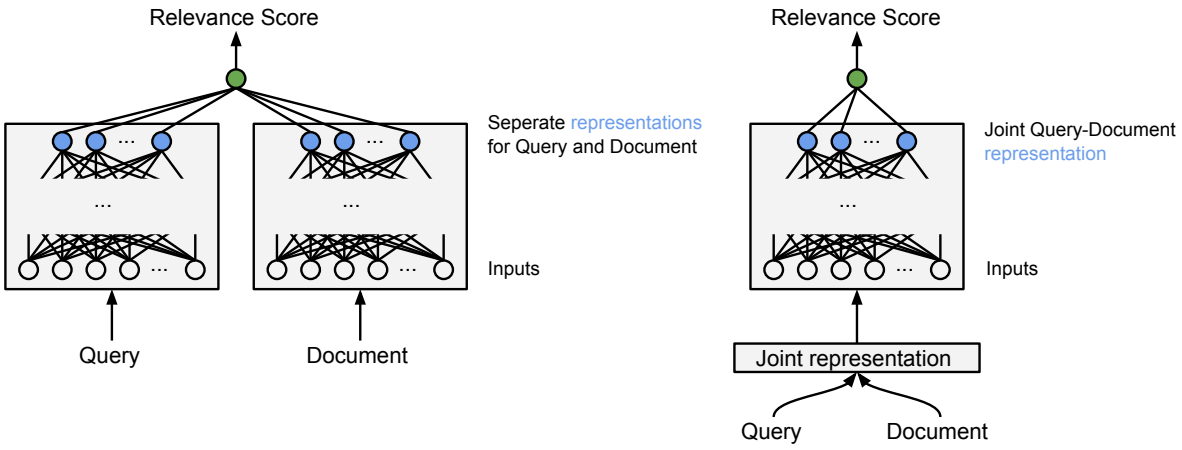


FIGURE 2.1: Example of a representation-focused model (left) and an interaction-focused model (right).

The representation-focused models build separate high level representations for the query and the document and then calculate a similarity score (e.g., cosine similarity) between the two representations, which is used as the relevance score of the document for the particular query. In many cases, the query and document representations are build using the same neural network independently, following the Siamese architecture paradigm (Bromley et al., 1993).

The interaction-focused models first build a joint representation of a query-document pair. This could be as simple as a matrix with the similarities of each query term to each document term. Then the joint representation passes through a neural network to produce a single relevance score of the document for the particular query.

Figure 2.1 illustrates the two categories using, for simplicity, a mirrored MLP for the representation-focused paradigm and a single MLP for the interaction-based one. However, any other architecture could be used to build the representations, for example recurrent (RNN) or convolutional (CNN) neural networks.

Although representation focused models are commonly used for various NLP problems, they fail to capture strong signals crucial to information retrieval like exact word matching, since they encode each document or query into a single high level representation. On the other hand, interaction-focused models are able to capture such strong signals early in the architecture and then apply neural operations on top of those signals. A drawback of the interaction-focused models is that the document representations cannot be indexed since documents have joint representations with queries, thus, a full forward step is required for each document during search time. As already mentioned, we will cope with this difficulty by using the neural network models for reranking, since the models that are presented in this work belong to the interaction-focused category.

Training Neural Networks for Information Retrieval

Training neural networks for document relevance ranking usually requires two forward propagations; one given as input a query q and a document d^+ where d^+ is relevant to the query q and one given as input the same query q and a document d^- not relevant to q. The neural network produces a relevance score $rel(q, d^+)$ for the first query-document pair (containing the relevant document) and a score $rel(q, d^-)$ for the second query-document pair (containing the non-relevant document). Two kinds of loss functions can then be used:

Hinge loss: Minimizing hinge loss aims to separate by a margin the scores assigned to the relevant and the non-relevant document given the same query, with the relevant document having the highest score among the two. In Eq. 2.3, the margin is set to 1, which is common.

$$\mathcal{L}(q, d^+, d^-; \Theta) = \max\{0, 1 - rel(q, d^+) + rel(q, d^-)\} \tag{2.3}$$

Negative log-loss: Minimizing negative log-loss aims to maximize the probability given to the relevant document that is obtained after applying a softmax function to $rel(q, d^+)$ and $rel(q, d^-)$.

$$\mathcal{L}(q, d^+, d^-; \Theta) = -log\left(\frac{\exp(rel(q, d^+))}{\exp(rel(q, d^+)) + \exp(rel(q, d^-))}\right) \tag{2.4}$$

The network parameters are then updated via a single backpropagation step, based on the selected loss.

2.3 The DRMM model

The Deep Relevance Matching Model (DRMM) of Guo et al., 2016, belongs to the interaction-focused category of document ranking neural networks, since it first calculates matching signals between query-document term pairs which are then passed to neural operations that produce a relevance score. DRMM takes as input a query q:

$$q = \{w_1^{(q)}, w_2^{(q)}, \ldots, w_m^{(q)}\} \tag{2.5}$$

and a document d:

$$d = \{w_1^{(d)}, w_2^{(d)}, \ldots, w_n^{(d)}\} \tag{2.6}$$

where $w_i^{(q)}$ denotes the pre-trained word embedding of the i-th query term of a query with length m and $w_i^{(d)}$ is the pre-trained word embedding of the i-th query term of a query with length n. Given these inputs DRMM produces the relevance score for the query-document pair using three basic components: Matching Histogram Mapping, Feed Forward Matching Network and the Term Gating Network. The basic architecture of DRMM is illustrated in Figure 2.2.

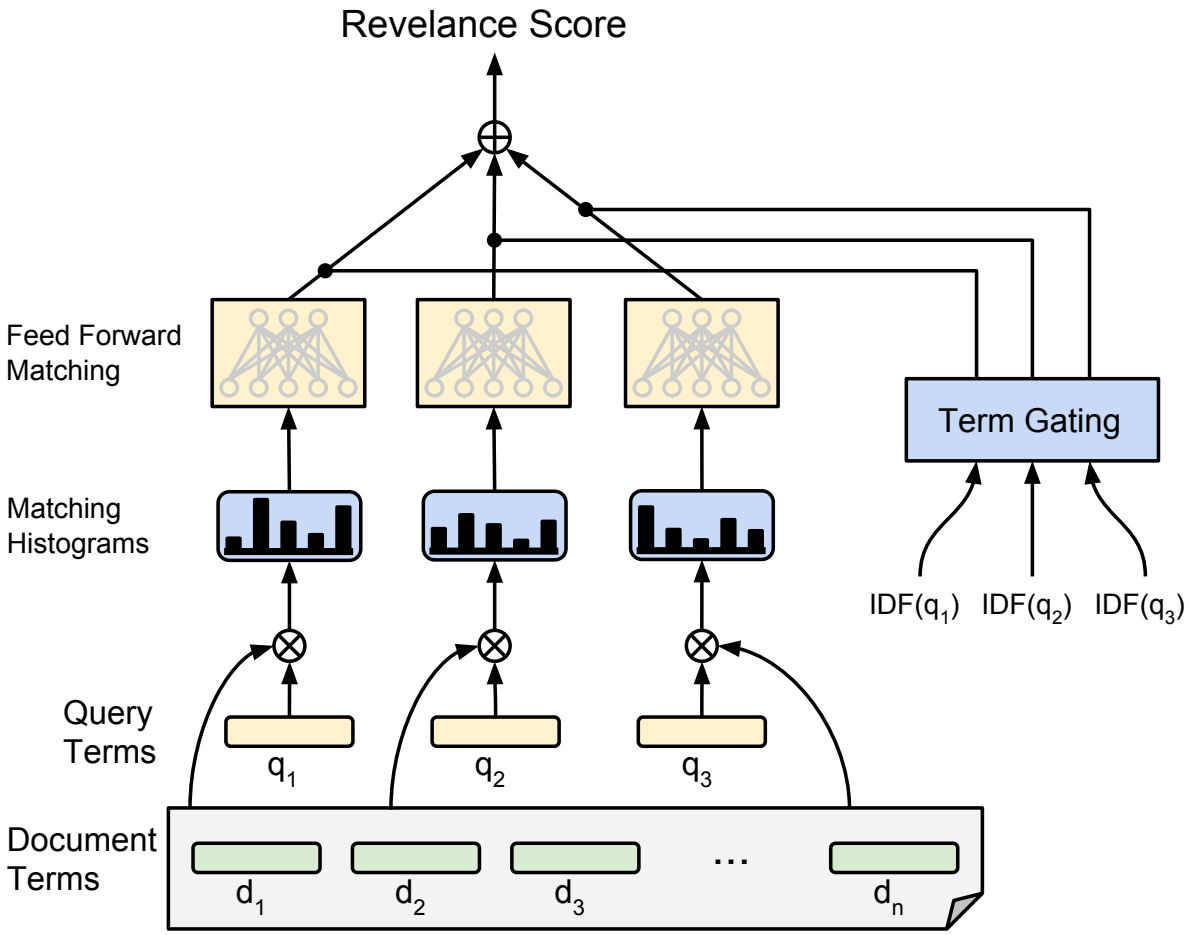


FIGURE 2.2: DRMM architecture for a query with 3 terms, a document with n terms, histograms of 5 bins and IDF based term gating.

Matching Histogram Mapping

This component transforms a pair consisting of a single query term and the entire document into a fixed-size histogram of similarities. More specifically, for a query term q_i the cosine similarity of its word embedding $w_i^{(q)}$ and the word embeddings of each document term $w_1^{(d)} \dots w_n^{(d)}$ is calculated resulting in a similarity vector of n-dimensions (not shown in Figure 2.2). Subsequently, this similarity vector is transformed into a fixed-length matching histogram. First the range of similarities, which is $[-1, 1]$ in the case of cosine similarity, is discretized into equal sized bins. Then each similarity score is assigned to the corresponding bin. Moreover, an additional bin is used for the scores that are exactly 1. For example, with a bin size of 0.5 the resulting bins would be $\{[-1, -0.5), [-0.5, 0), [0, 0.5), [0.5, 1), [1, 1]\}$. This process is repeated for each query term. These matching histograms can be presented in three ways:

- **Count-based Histogram (CH):** Each bin keeps the count of the similarity scores that lie in its range (as described above).
- **Normalized Histogram (NH):** The count of each bin is normalized by dividing it by the sum of the counts of all bins.

- **LogCount-based Histogram (LCH):** A logarithm is applied to the CH count of each bin.

Feed Forward Matching Network

Each query term matching histogram, then passes through a Multi-Layer Perceptron (the same for all histograms), in order to produce a matching score for each query term.

Term Gating Network

At this point a simple summation of the query term matching scores could be used to produce the query-document relevance score. However, DRMM deploys a term gating network to weight each term matching score based on query term importance. There are two ways to produce these gating weights g_i, both using linear self-attention:

$$g_i = \frac{\exp\left(w_g^T x_i^{(q)}\right)}{\sum_{j=1}^{M} \exp\left(w_g^T x_j^{(q)}\right)} \tag{2.7}$$

- **Inverse Document Frequency (IDF):** In the simplest case, $x_i^{(q)}$ is the IDF of the i-th query term and w_g is a single parameter (scalar weight).
- **Term Vector (TV):** In this case, $x_i^{(q)}$ is the word embedding of the i-th query term and w_g is a weight vector of the same dimensionality.

Since experimental results of Guo et al., 2016 suggest that DRMM performs best using LogCount-based Histograms (LCH) and Inverse Document Frequency (IDF) term gating, only this setup of the model will be used ($\text{DRMM}_{LCH \times IDF}$) which for simplicity will be called DRMM.

Training

Having the relevance scores $rel(q, d^+)$, $rel(q, d^-)$ produced by the forward propagations for a query q, a relevant document d^+ and a non-relevant document d^-, hinge-loss (Eq. 2.3) is then applied to these scores and the model's parameters are updated via backpropagation using the Adam optimizer (Kingma and Ba, 2014).

2.4 The PACRR model

Hui et al. (2017) proposed the Position-Aware Convolutional-Recurrent Relevance matching model (PACRR), an interaction-focused neural network model which aims to capture position-dependent interactions between a query and a document.

Architecture

Similarly to DRMM, PACRR takes as input a query

$$q = \{w_1^{(q)}, w_2^{(q)}, \ldots, w_{|q|}^{(q)}\} \tag{2.8}$$

and a document

$$d = \{w_1^{(d)}, w_2^{(d)}, \ldots, w_{|d|}^{(d)}\} \tag{2.9}$$

where $w_i^{(q)}$ denotes the pre-trained word embedding of the i-th query term of a query q with length $|q|$ and $w_i^{(d)}$ the pre-trained word embedding of the i-th query term of a document d with length $|d|$.

First, the query is zero padded to fit a fixed maximum length l_q. Similarly, the document is zero padded if it is shorter than a fixed maximum length l_d. If it is longer, the first l_d document terms are kept (this strategy is called PACRR-firstk by Hui et al., 2017).

Then, PACRR converts the query-document pair into a similarity matrix $sim_{l_q \times l_d}$, where $sim_{i,j}$ represents the cosine similarity between the i-th query term's word embedding and the j-th document term's word embedding:

$$sim_{i,j} = \frac{w_i^{(q)^T} w_j^{(d)}}{||w_i|| \cdot ||w_j||} \tag{2.10}$$

Convolution relevance matching over local text snippets

After the construction of $sim_{l_q \times l_d}$, PACRR applies two-dimensional convolutional filters of various kernel sizes $(n \times n), n = 2, \ldots l_g$ to this similarity matrix, where l_g is the maximum size of the convolutional filters ($l_g \leq l_q$) and is treated as a hyperparameter. The purpose of these filters is to capture similarity matching beyond *uni*-grams. Intuitively, each filter size $(2 \times 2), (3 \times 3), \ldots, (l_g \times l_g)$ captures *bi*-gram, *tri*-gram, ..., l_g-gram similarities respectively. For each filter size multiple filters are applied. The number of filters per filter size is denoted as n_f and is common for all filter sizes. The outputs of these (wide) convolutions are the matrices $C^2_{l_q \times l_d \times n_f}, \ldots, C^{l_g}_{l_q \times l_d \times n_f}$ where the exponent $2, \ldots, l_g$ corresponds to the size of the filter resulting to this matrix. The *uni*-gram similarities are captured by the original matrix $sim_{i,j}$ which for uniformity is now denoted as $C^1_{l_q \times l_d \times 1}$, although it is not the result of a convolution.

Pooling Layers

Subsequently, max pooling is applied to the n_f dimension of each matrix $C^2_{l_q \times l_d \times n_f} \dots C^{l_g}_{l_q \times l_d \times n_f}$ to keep the strongest signal among those produced by the multiple (n_f) filters of a certain size. This process results to the matrices $C^2_{l_q \times l_d \times 1} \dots C^{l_g}_{l_q \times l_d \times 1}$. At this point, each row i of each matrix $C^1_{l_q \times l_d \times 1}, C^2_{l_q \times l_d \times 1} \dots C^{l_g}_{l_q \times l_d \times 1}$ represents the relevance of the corresponding (i-th) query term with the document at *uni-gram*, *bi-gram*, ..., l_g-*gram* level respectively. As a second pooling strategy, k-max pooling is applied to each row of each matrix, keeping the strongest k signals, resulting to the matrices $P^1_{l_q \times k}, \dots, P^{l_g}_{l_q \times k}$. Finally, these matrices are concatenated on the k dimension to create the matrix $P_{l_q \times (l_g \cdot k)}$.

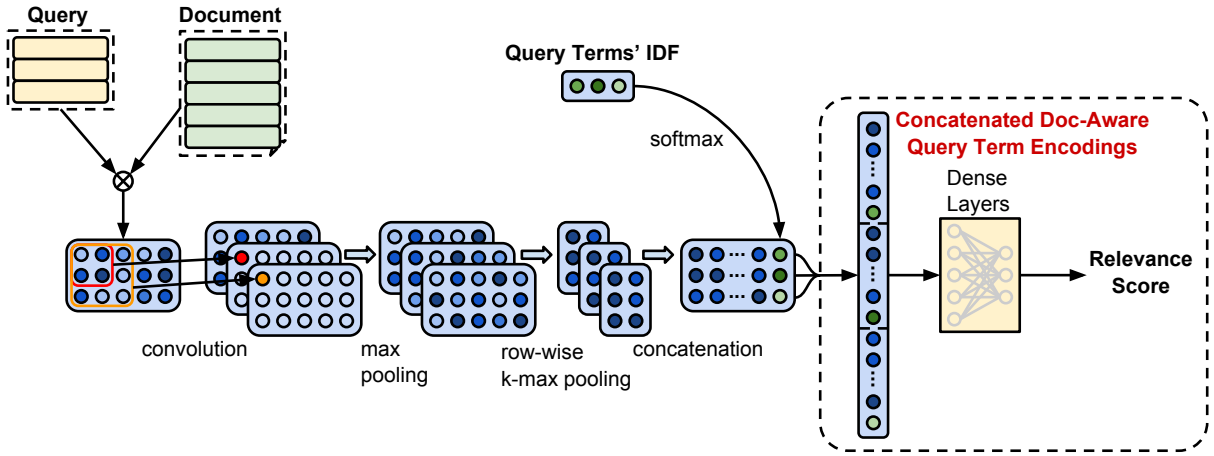


FIGURE 2.3: PACRR architecture.

IDF weighed representations

Now, each row i of matrix $P^1_{l_q \times (l_g \cdot k)}$ is a document aware representation of the i-th query term. The IDF scores of the query terms are also appended in the corresponding rows, after normalizing them through softmax, in order to indicate the importance of each query term.

Document Scoring Layer

Since now every query term has a document aware representation vector, what is left is a layer to combine these representations into a single relevance score. This can be achieved by using one of the following components:

Recurrent Layer: Each query term vector representation is passed through a Long-Short Term Memory (LSTM) recurrent layer (Hochreiter and Schmidhuber, 1997) with output dimensionality of one, in order to produce the final relevance score of the query-document pair. This was the original version of PACRR proposed by Hui et al., 2017. We will refer to this variation of the model as PACRR-RNN.

Multi-Layer Perceptron (MLP): Hui et al. (2018), in an improved version of PACRR, proposed the replacement of the recurrent layer with a Multi-Layer Perceptron (MLP). This MLP takes as input the concatenation of all query term representations and produces a single number which represents the query-document relevance score, as shown in Figure 2.3. We will refer to this variation simply as PACRR.

Term specific Multilayer Perceptron: As a third option, we investigate the use of an MLP which operates on top of each query term representation (the same MLP for all representations) and produces a relevance score for each query term. Then, these scores are combined linearly to produce a final query-document relevance score. We will refer to this variation as TERM-PACRR.

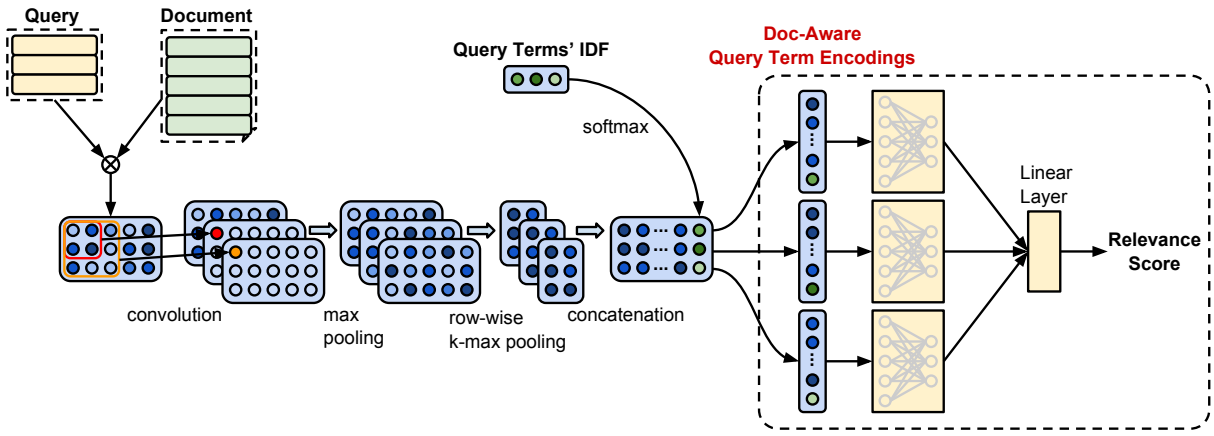


FIGURE 2.4: TERM-PACRR architecture.

Training

Similarly to DRMM, the training process requires a query q, a relevant document d^+ and a non-relevant document d^-. After having the relevance scores $rel(q, d^+)$, $rel(q, d^-)$ produced by the forward propagations, softmax is applied and negative log-loss is calculated for the (softmax) normalized score of the relevant document (Eq. 2.4), when the improved PACRR version of Hui et al., 2018 is used. The original PACRR model (Hui et al., 2017) used a pair-wise hinge loss, which in early experiments seemed to provide similar performance. Finally, the model parameters are updated in a single backpropagation step, using the Adam optimizer (Kingma and Ba, 2014).

2.5 Extra features for exact match capturing

As an attempt to improve the reranking performance we will include the BM25 score of the document as an extra input to the deep relevance ranking models. Having a query q and a list of top N retrieved documents to be reranked, we normalize the BM25 scores of these documents using z-normalization as shown in Eq. 2.11, where μ, σ are the mean and standard deviation of the BM25 scores of the documents in the list respectively, s_i is the BM25 score of the i-th retrieved document and z_i is the normalized score of this document which will be used as input to the models.

$$z_i = \frac{s_i - \mu}{\sigma} \tag{2.11}$$

Moreover, we will add three additional features that aim to provide strong signals of exact uni-gram or bi-gram matching between a query-document pair. Specifically, we will use three overlap features (Severyn and Moschitti, 2015; Mohan et al., 2017):

Uni-gram overlap ($overlap_1$): Given the set of distinct tokens U_q for a query and the set of distinct tokens U_d for a document, uni-gram overlap is the number of common tokens between the two sets, divided by the number of tokens in U_q (Eq. 2.12).

$$overlap_1 = \frac{|U_q \bigcap U_d|}{|U_q|} \tag{2.12}$$

Bi-gram overlap ($overlap_2$): Given the set of distinct bi-grams B_q for a query and the set of distinct bi-grams B_d for a document, bi-gram overlap is the number of common bi-grams between the two sets, divided by the number of bi-grams in B_q (Eq. 2.13).

$$overlap_2 = \frac{|B_q \bigcap B_d|}{|B_q|} \tag{2.13}$$

IDF weighted uni-gram overlap ($overlap_3$): Given the set of distinct uni-grams U_q for a query and the set of distinct bi-grams U_d for a document, IDF weighted uni-gram overlap is the sum of the IDF values of the common uni-grams between the two sets, divided by the sum of the IDF values of the uni-grams in U_q (Eq. 2.14).

$$overlap_3 = \frac{\sum_{t \in U_q \bigcap U_d} IDF(t)}{\sum_{t \in U_q} IDF(t)} \tag{2.14}$$

Using extra features with neural ranking models.

We will introduce the extra features to the DRMM model by linearly combining them with the relevance score produced by DRMM as visualized in Figure 2.5 (A).

For the PACRR model, we will append the extra features to the document aware concatenated term representations as shown in Figure 2.5 (B). Then, extra features are passed to the MLP as part of this concatenated vector. Finally, for the TERM-PACRR model we will include the

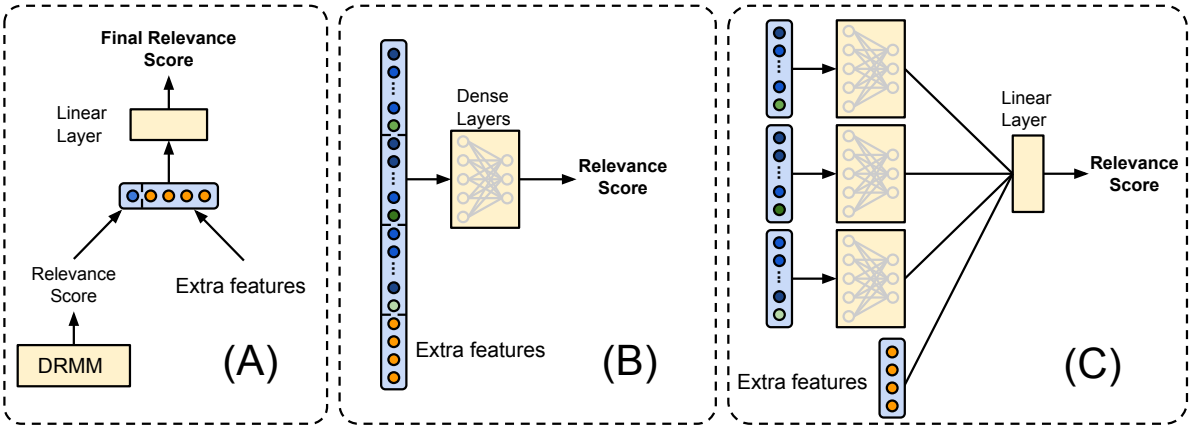


FIGURE 2.5: Using extra features with DRMM (A), PACRR (B) and TERM-PACRR (C)

extra features to the linear combination of the document aware term scores produced by the MLP as in Figure 2.5 (C).

The extra linear layer that was used for DRMM could also be used with PACRR and TERM-PACRR. However, experimental results suggested that the proposed strategies provide slightly better performance.

We will refer to the models that use the BM25 feature as DRMM-BM25, PACRR-BM25 and TERM-PACRR-BM25. Similarly, models that use the overlap features will be referred as DRMM-OL, PACRR-OL, TERM-PACRR-OL and models that use both the BM25 and the overlap features as DRMM-EXTRA, PACRR-EXTRA, TERM-PACRR-EXTRA.

Chapter 3

Experiments

3.1 Data

The main evaluation of the methods described in this work utilize data provided by the BIOASQ challenge (Tsatsaronis et al., 2015). Methods are also evaluated on the TREC ROBUST 2004 dataset (Voorhees, 2005) to confirm the consistency of the experimental results.

3.1.1 BioASQ dataset

The BioASQ challenge

BIOASQ is a biomedical semantic indexing and question answering (QA) challenge, which started as a project funded by the European Union (2012-14)[1], and is now supported by the U.S. National Library of Medicine of the National Institutes of Health[2]. The annual challenges, currently in the 6^{th} year (2018), include hierarchical text classification, information retrieval, QA from texts and structured data as well as text summarization and other tasks.

The challenge is structured in two independent tasks[3]:

- **Task A: Large-Scale Online Biomedical Semantic Indexing**
  Participants are asked to classify new PubMed abstracts into classes from the MeSH hierarchy[4].
- **Task B: Biomedical Semantic QA:**
  This task includes IR, QA and summarization. Participants are given a training dataset containing biomedical questions with annotated answers and relevant information and are asked to respond to new test questions in two phases:
  - phase A: Participants respond with relevant documents, snippets, concepts and RDF triples from designated sources. In particular, at most 10 relevant documents should be returned for each question, in decreasing order of relevance. At most 10 relevant snippets should be extracted from the 10 predicted relevant documents, also in decreasing order of relevance. This information is available during training.

[1] https://cordis.europa.eu/project/rcn/105774_en.html
[2] https://www.nlm.nih.gov/
[3] For more information on the tasks, see: http://bioasq.org/participate/challenges
[4] See https://www.nlm.nih.gov/mesh/

– phase B: After the completion of phase A, gold relevant documents of the test queries are made available for phase B and participants are asked to respond with exact answers (e.g. named entities in the case of factoid questions) and ideal answers (paragrapsh-sized summaries).

A first evaluation of the participating systems is based of these gold documents. A second stage of manual evaluation (by biomedical experts) produces the final ranking of the systems. During the manual evaluation, the experts add to the gold documents, snippets, answers etc. any system responses that were correct and were not originally included in the gold ones.

Dateset description

For training and development of the models we will use the Task6b-phase A training data from the 6^{th} BIOASQ challenge which contain 2251 English questions of biomedical interest and a list of documents for each question which are marked as relevant by biomedical experts, among other annotated information (e.g. snippets) that are not directly relevant to this work.

The methods will then be used to predict relevant documents for the 500 queries (five batches of 100 queries) of the test data of the 6^{th} year of BIOASQ. For their evaluation, the gold documents of phase B will be used. We will refer to the BIOASQ test dataset as BIOASQ6-TEST and to a test batch B in particular as BIOASQ6TEST-BATCH-B.

For the purposes of our experiments we further split the 2251 queries of the 'training' dataset of the 6^{th} year of BIOASQ into train and development sets so that the training set (BIOASQ6-TRAIN) contains the 1751 queries corresponding to training queries created up to the 5^{th} year of BIOASQ and the development set (BIOASQ6-DEV) contains the 500 queries added to the 'training' set for the 6^{th} year, which were the test set of the 5^{th} year (Figure 3.1). Table 3.1 shows examples of BIOASQ queries.

	BIOASQ queries
1	In what proportion of children with heart failure has Enalapril been shown to be safe and effective?
2	Which polyQ tract protein is linked to Spinocerebellar Ataxia type 2?
3	What is the effect of amitriptyline in the mdx mouse model of Duchenne muscular dystrophy?
4	What is the outcome of TAF10 interacting with the GATA1 transcription factor?
5	Is there any association of the chromosomal region harboring the gene ITIH3 with schizophrenia?

TABLE 3.1: Examples of BIOASQ queries.

Dataset statistics

An important statistic for the document ranking task is the number of annotated (gold) relevant documents per query during training and development of the models for two reasons. First, the number of annotated relevant documents is proportional to the number of the extracted training examples, so more annotated relevant documents will most probably result to more training examples. An other reason is that a small number of annotated documents could lead

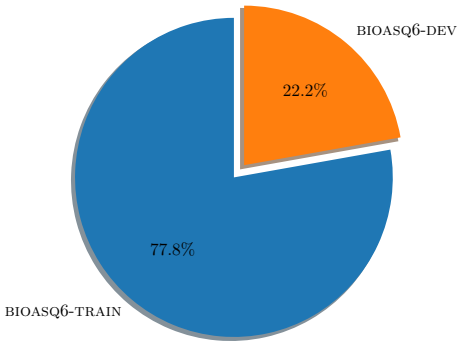


FIGURE 3.1: Percentage of BIOASQ6-TRAIN and BIOASQ6-DEV sets over the whole 'training' dataset provided by the BIOASQ6 phase A challenge.

to low performance scores on the development set due to retrieving (or ranking high) relevant documents that were not annotated by humans.

Table 3.2 reports statistics on the annotated relevant documents per query for BIOASQ6-TRAIN and BIOASQ6-DEV and each batch of the BIOASQ6-TEST dataset. Moreover, Figure 3.2 illustrates the frequency of relevant document counts over the queries of each set.

Relevant documents per query	BIOASQ6 TRAIN	BIOASQ6 DEV	BIOASQ6-TEST				
			Batch1	Batch2	Batch3	Batch4	Batch5
Average	12.0	11.9	4.1	3.8	4.0	3.4	3.9
Standard Deviation	10.9	11.6	3.0	3.1	3.2	2.7	2.8
Minimum	1	1	1	1	1	1	1
Maximum	157	86	13	13	14	16	13
Mode	8	1	1	1	1	1	1

TABLE 3.2: Statistics about the number of relevant documents per query, for BIOASQ6-TRAIN, BIOASQ6-DEV and each batch (1-5) of the BIOASQ6-TEST dataset.

It can be observed that queries of the BIOASQ6-TEST set have fewer annotated relevant documents in comparison to BIOASQ6-TRAIN and BIOASQ6-DEV. This happens because at the end of each year's challenge, relevant documents found during human evaluation are added to the gold set for the next year's training data. Moreover, up to the 4^{th} year of the challenge, annotators were told to mark all relevant documents found. For the subsequent years, the minimum number of documents needed to answer a query would suffice, which explains why most queries in BIOASQ6-DEV (year 5) have only 1 annotated relevant document.

As already mentioned the queries of this dataset are in the form of English questions (not just keywords). Table 3.3 shows statistics about the length of the queries for each BIOASQ set.

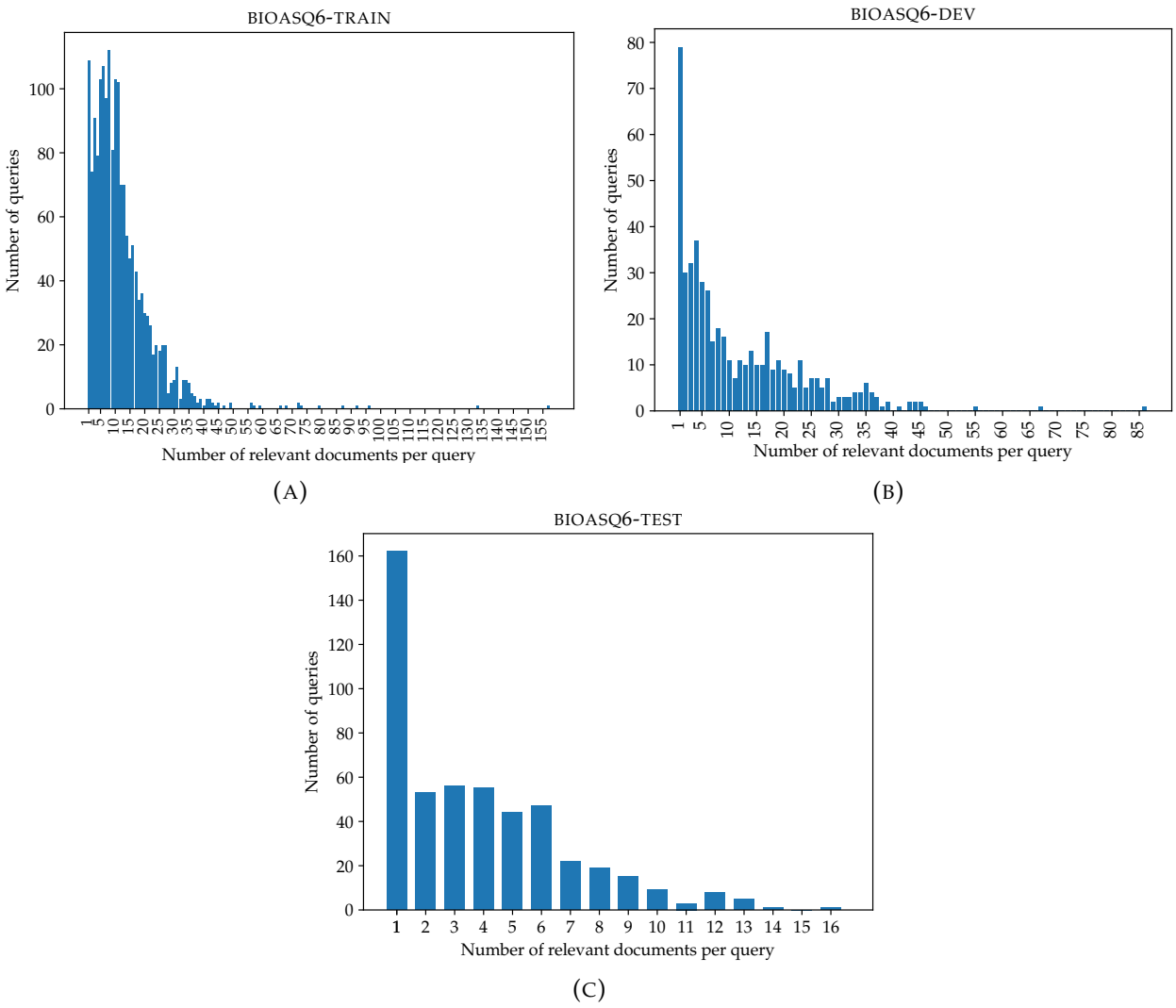


FIGURE 3.2: Histograms showing the frequency of annotated relevant document counts over the queries of BIOASQ6-TRAIN (A), BIOASQ6-DEV (B) and BIOASQ6-TEST (C).

Query length in tokens	BIOASQ6 TRAIN	BIOASQ6 DEV	BIOASQ6-TEST				
			Batch1	Batch2	Batch3	Batch4	Batch5
Average	9.4	8.2	8.8	8.6	8.3	7.4	8.3
Standard Deviation	3.2	3.1	3.1	3.0	4.1	3.2	3.4
Minimum	3	2	3	3	2	2	3
Maximum	30	27	22	18	21	22	19
Mode	9	8	8	8	8	6	8

TABLE 3.3: Statistics about the queries' length in tokens, for BIOASQ6-TRAIN, BIOASQ6-DEV and each batch (1-5) of the BIOASQ6-TEST dataset.

Document Collection

Following the BIOASQ challenge's guidelines, the document collection that will be used for searching derives from the MEDLINE/PubMed Baseline Repository 2018 (January), containing approximately 28 million biomedical articles. For 18 million of those there is title and abstract available (among various other fields), while for the other 10 million only the title is available (see Table 3.4).

Number of articles	27,836,723
Number of articles with title and abstract	17,730,230
Number of articles with title only (no abstract)	10,106,493

TABLE 3.4: Document collection statistics.

Since articles with only title available might not contain enough information for a document retrieval task, we choose to discard those 10 million documents and reduce our search space to 18 million documents with both title and abstract. Moreover, the number of gold articles of the training set without an abstract available is 95 (0.35%) which indicates that this choice will not affect the development process. During experiments we treat the concatenation of the title and the abstract as a document, having on average a length of 196.6 tokens. IDF values used during the experiments were calculated on these 18 million documents.

At this point, we should mention that since the dataset consists of queries added in previous years of the challenge, the annotators of older queries did not have access to documents published later, i.e., more recent documents contained in the PubMed 2018 collection that we use for retrieval, that might be relevant to a query. In order to simulate these conditions for our training and development stage, we remove from the top N retrieved documents, those published after 2015 for the training set, and those published after 2016 for the development set.

Pre-processing and tokenization

The text of each biomedical article was pre-processed and tokenized using the *bioclean* function provided by BIOASQ as part of their released pre-trained biomedical word embeddings[5]. It is simply a regular expression that removes various special symbols (e.g. [.,?;!%()]) and then splits text by the space character. The dash (-) character is not removed in order to capture complex biomedical terminology (e.g. *ca2-calmodulin-proteinkinase*).

Pre-trained word embeddings.

For pre-trained word embeddings, we trained WORD2VEC (Mikolov et al., 2013) over the 28 million biomedical articles of the MEDLINE/PubMed Baseline Repository 2018, using both the titles and the abstracts (if available). All abstracts were split into sentences using the sentence splitter of *NLTK*[6]. All sentences and titles were then preprocessed and tokenized using

[5]The *bioclean* function accompanies the biomedical word embeddings of BIOASQ available at: http://participants-area.bioasq.org/tools/BioASQword2vec/

[6]http://www.nltk.org/api/nltk.tokenize.html (v. 3.2.3)

the *bioclean* function. After applying WORD2VEC to the preprocessed and tokenized titles and sentences, we obtained biomedical word embeddings of 200 dimensions. [7] Early experiments indicated that there is no noticeable performance difference when using larger dimensions. Detailed WORD2VEC related statistics of the corpus used are shown in Table 3.5. Tools and hyper-parameters used for WORD2VEC are reported in the experimental setup (Section 3.3).

Number of articles	27,836,723
Number of articles with title and abstract	17,730,230
Number of articles with title only (no abstract)	10,106,493
Number of sentences	173,755,513
Number of tokens	3,580,134,037
Average sentence length (tokens)	20.6

TABLE 3.5: WORD2VEC training corpus statistics. Titles are treated as sentences.

BIOASQ data augmentation via translation

Neural networks often benefit from more training data. Thus, a next step for improvement is to augment the BIOASQ training dataset. As a first approach we will attempt augmentation by translating text to an other language and then back to the original (English). Empirically, we have found that the presented models benefit from more training queries rather than more annotated relevant documents per query. Thus, we will double the number of training queries in BIOASQ6-TRAIN using augmentation via translation on its queries. We expect that translating a query to an other language and then back to English will result to an alternative form of it, having the same or very similar meaning to the original, using different words and/or phrases. For each artificial query we use as annotated relevant documents those of the original. In total, three translating scenarios will be considered:

- EN-DE-EN: English → German → English
- EN-JA-EN: English → Japanese → English
- EN-JA-DE-EN: English → Japanese → German → English

Examples of five randomly selected queries shown in Table 3.6 indicate that using this augmentation method leads to good paraphrasing of the original query by replacing words (e.g. *proportion* → *percentage*, *outcome* → *result*) or phrases (e.g. *has Enalapril been shown to be safe* → *has it been shown that enalapril is safe*) and/or changing their order.

[7] Our biomedical embeddings, which are not the same as the ones provided by BIOASQ, are available from: http://nlp.cs.aueb.gr/software.html

Augmentation	Output Query
	Query 1
-	In what proportion of children with heart failure has Enalapril been shown to be safe and effective?
EN-DE-EN	In which proportion of children with heart failure has it been shown that enalapril is safe and effective?
EN-JA-EN	At what percentage of children with heart failure, is Enalapril shown to be safe and effective?
EN-JA-DE-EN	In what percentage of children with heart failure is enalapril safe and effective?
	Query 2
-	Which polyQ tract protein is linked to Spinocerebellar Ataxia type 2?
EN-DE-EN	Which PolyQ tract protein is associated with spinocerebellar ataxia type 2?
EN-JA-EN	What polyQ tract protein is associated with type 2 spinocerebellar ataxia?
EN-JA-DE-EN	Which PolyQ tract protein is associated with spinocerebellar ataxia type 2?
	Query 3
-	What is the effect of amitriptyline in the mdx mouse model of Duchenne muscular dystrophy?
EN-DE-EN	How does amitriptyline work in the mdx mouse model of Duchenne muscular dystrophy?
EN-JA-EN	What is the effect of amitriptyline on the mdx mouse model of Duchenne muscular dystrophy?
EN-JA-DE-EN	How does amitriptyline affect the mdx mouse model of Duchenne muscular dystrophy?
	Query 4
-	What is the outcome of TAF10 interacting with the GATA1 transcription factor?
EN-DE-EN	What is the result of the interaction of TAF10 with the GATA1 transcription factor?
EN-JA-EN	What is the result of TAF 10 interacting with the GATA1 transcription factor?
EN-JA-DE-EN	What is the result of the interaction of TAF 10 with the GATA1 transcription factor?
	Query 5
-	Is there any association of the chromosomal region harboring the gene ITIH3 with schizophrenia?
EN-DE-EN	Is there an association of the chromosomal region harboring the gene ITIH3 with schizophrenia?
EN-JA-EN	Is there an association between schizophrenia and chromosomal region with gene ITIH3?
EN-JA-DE-EN	Is there a connection between schizophrenia and the chromosomal region with the gene ITIH3?

TABLE 3.6: Examples of augmented BIOASQ queries using translation.

3.1.2 TREC Robust2004 dataset

The second dataset that we will use is the TREC ROBUST 2004 dataset (Voorhees, 2005) which is widely used to evaluate conventional ad-hoc retrieval systems and recent neural models like DRMM (Guo et al., 2016).

Dataset description

TREC ROBUST 2004 contains 250 queries with annotated relevant documents. Each query has two fields; a title and a description. For this work we will use only the title of each query. Examples of these queries are shown in Table 3.7[8]. Due to the limited number of queries, we will use 5-fold cross validation by splitting the dataset into five parts containing 50 queries each. For each fold, $\frac{3}{5}$ of the queries are used for the training process, $\frac{1}{5}$ for development and the remaining $\frac{1}{5}$ for testing, so that each part is used in exactly one fold for testing and one fold for development. Systems are then evaluated by calculating the macro-average of each measure across the five folds.

	ROBUST 2004 queries
1	agoraphobia
2	telemarketer protection
3	alzheimer's drug treatment
4	journalist risks
5	add diagnosis treatment

TABLE 3.7: Examples of ROBUST 2004 queries (title field).

Dataset statistics

Since every query is used for training, development and testing during cross-validation, the following statistics are reported over the whole set of 250 queries. Table 3.8 reports statistics about the number of annotated relevant documents per query while Figure 3.3 shows the frequency of each of the annotated relevant documents counts, which in this case fluctuates a lot. The fact that there are significantly more annotated documents per query, in comparison with BIOASQ, helps to produce enough training examples given the very small number of queries.

Relevant documents per query	ROBUST 2004
Average	69.6
Standard Deviation	74.4
Minimum	0
Maximum	448
Mode	16

TABLE 3.8: Statistics about the number of relevant documents per query, for ROBUST 2004.

[8]Since these queries are more similar to keyword queries rather than natural language ones, we will not experiment with augmentation via translation as we did for the BIOASQ queries.

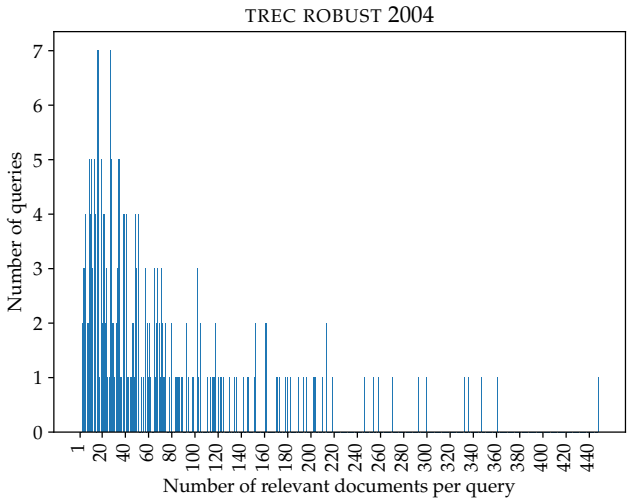


FIGURE 3.3: Histogram showing the frequency of annotated relevant document counts over the queries of TREC ROBUST 2004.

Statistics regarding the length of the queries are available in Table 3.9 showing that the queries are much shorter than those of BIOASQ.

Query length in tokens	ROBUST 2004
Average	2.7
Standard Deviation	0.7
Minimum	1
Maximum	5
Mode	3

TABLE 3.9: Statistics about the query length in tokens, for TREC ROBUST 2004.

Document collection

The document collection of this dataset consists of about 528K documents. These documents originate from four different corpora, namely *Financial Times*, *Federal Register 94s*, *FBIS* and *LA Times*. IDF values used for the experiments where calculated on this collection. On average, each document has a length of 476.5 tokens.

Pre-processing and tokenization The documents were preprocessed by first removing *HTML* tags and irrelevant corpus specific fields. Then a regular expression was used to remove special characters like [.?!%()-] and then text was split to tokens using *NLTK*'s word tokenizer. [9] Due to their keyword-like nature, queries required minimal preprocessing.

Pre-trained word embeddings.

For pre-trained word embeddings, we trained WORD2VEC over the 528K document collection. All documents were split into sentences using the sentence splitter of *NLTK*. All sentences were

[9] http://www.nltk.org/api/nltk.tokenize.html (v. 3.2.3)

then preprocessed and tokenized. After applying WORD2VEC to the preprocessed and tokenized sentences, we obtained word embeddings of 200 dimensions (see Section 3.3).

3.2 Evaluation Measures

In this section we describe the measures that we will use to evaluate the systems.[10] Starting from standard IR measures (Manning et al., 2008), we will then provide further details about the evaluation measures of BIOASQ and TREC ROBUST 2004.

Standard IR measures

All measures require a set of gold (relevant) documents and a list of documents returned by a system, for each query. Given this information we will first define two basic measures; *Precision* (P) and *Recall* (R):

$$P = \frac{TP}{TP + FP} \tag{3.1}$$

$$R = \frac{TP}{TP + FN} \tag{3.2}$$

where TP (True Positives) is the number of returned documents that are present in the gold set (relevant documents), FP (False Positives) is the number of returned documents that are not present in the gold set and FN (False Negatives) is the number of documents that are present in the gold set but not in the returned list.

Precision and *Recall* do not take into account the order of the documents in the list returned by a system which is crucial in IR (relevant documents should appear first in the list of returned documents of a search engine). Average Precision (AP) takes into account the position of the returned documents in the list of results, to score the performance on a single query:

$$AP = \frac{\sum_{r=1}^{|L|} P(r) \cdot rel(r)}{|L_R|} \tag{3.3}$$

where $|L|$ is the number of documents returned by the system, $P(r)$ is the precision of the system when only the top r returned documents are considered, $|L_R|$ is the number of documents in the gold set and $rel(r)$ is 1 if the document positioned r-th is annotated as relevant, else 0.

For a set of queries Q, Mean Average Precision (MAP) is the mean of AP over the queries:

$$MAP = \frac{1}{|Q|} \cdot \sum_{i=1}^{|Q|} AP_i \tag{3.4}$$

[10] The description of some measures follows closely Malakasiotis et al., 2018; see also: http://participants-area.bioasq.org/Tasks/b/eval_meas_2018/

BioASQ evaluation measures

For the BIOASQ evaluation we will stick with the official evaluation measures of the challenge, listed below. Since BIOASQ requires a maximum of 10 documents to be returned for each query, all measures are calculated on the top 10 (or less) documents:

- $MAP^{\star}$
  The MAP measure modified so that AP is calculated with L_R fixed to 10, since the maximum size of the returned list $|L|$ can be up to 10 and most queries have at least 10 gold documents. However if a query has less than 10 gold documents, the system is wrongly penalized. The notation $MAP^{\star}$ is used to avoid confusion between this and the original definition of MAP. $MAP^{\star}$ is the official system ranking score of the challenge and systems' comparison in this work will be mainly based on it.

- $GMAP$
  The Geometric Mean Average Precision ($GMAP$) is similar to MAP but uses the geometric mean which places more emphasis on improvements in low performing queries. A very small number ϵ is used to cover the case where average precision is zero.

$$GMAP = \sqrt[n]{\prod_{i=1}^{n}(AP_i + \epsilon)} \tag{3.5}$$

- *Precision* as defined in Equation 3.1.

- *Recall* as defined in Equation 3.2.

- *F-measure* (or F_1)
  The harmonic mean of *Precision* (P) and *Recall* (R):

$$F\text{-}measure = 2 \cdot \frac{P \cdot R}{P + R} \tag{3.6}$$

When used for a set of queries, *Precision*, *Recall* and *F-measure* are calculated as the macro-average of the corresponding measure along the queries.

A critical peculiarity of the BIOASQ dataset is that the annotated documents for a query are relatively limited and given the very large number of articles, it is possible that many relevant documents are not examined and annotated. This results to penalizing systems that succeed to retrieve these documents. In an attempt to moderate this problem, we suggest an additional evaluation technique based on already defined measures. It is a *Recall@k* curve constructed by plotting the recall of a system (y-axis) calculated up to the top k returned documents, for different values of $k = 1, 2, \ldots, N$ (x-axis). This way, whenever k increases by 1, *Recall@k* increases if an additional annotated relevant document is included in the top k, else remains the same without penalizing the system for possibly including a non-annotated relevant document as any precision based measure like MAP would do. We can also extract a single score by

approximating the Area Under Recall@k ($AUR@k$) as follows:

$$AUR@k = \frac{1}{N} \cdot \sum_{k=1}^{N} Recall@k \tag{3.7}$$

For completeness, we can similarly plot a *Precision@k* curve and obtain Area Under Precision@k ($AUP@k$) as follows:

$$AUP@k = \frac{1}{N} \cdot \sum_{k=1}^{N} Precision@k \tag{3.8}$$

TREC Robust 2004 evaluation measures

The evaluation on TREC ROBUST 2004 will utilize standard IR measures, instead of the BIOASQ measures that were designed based on dataset peculiarities, and will be calculated on the list of top 1000 documents returned by each system, unless otherwise stated. The selected measures have been used in previous works using this dataset, like the one of Guo et al., 2016. These are:

- *MAP*
  The standard definition of Mean Average Precision calculated on the whole list of 1000 documents.
- *Precision*@20
  Precision calculated on the top 20 documents in the returned list.
- *nDCG*@20 The normalized discounted cumulative gain designed mostly for non binary relevance predictions is defined as follows:

$$nDCG(Q,k) = \frac{1}{|Q|} \cdot \sum_{j=1}^{|Q|} Z_{kj} \sum_{i=1}^{k} \frac{2^{R(j,i)} - 1}{log_2(1+m)} \tag{3.9}$$

  where Q is a set of queries, $R(j,i)$ is the relevance score of the i-th retrieved document for a query j (in our case 0 or 1), Z_{kj} is a normalization factor corresponding to a perfect ranking's discounted cumulative gain and k is an upper threshold of retrieved documents. In $nDCG@20$, $k = 20$.

Pair-wise ranking evaluation

Apart from the standard IR measures we also used an additional measure to evaluate the ability of a system to score a relevant document higher than a non-relevant given a query. The *pair-wise ranking Accuracy* or simply *Accuracy* is calculated over triplets (Q, d^+, d^-) as follows:

$$Accuracy = \frac{\#triplets : rel(q,d^+) > rel(q,d^-)}{\#triplets} \tag{3.10}$$

where d^+ is a relevant and d^- a non-relevant document to a query q. This measure was used mostly for evaluation on the training and development sets over epochs of training, to help with model selection and hyper-parameter tuning.

3.3 Experimental Setup

3.3.1 Initial document retrieval

The first step of the experimental pipeline is to retrieve N documents for each query. For this purpose, we used the *Galago*[11] search engine with its scoring function set to BM25, a relatively simple but powerful method described in Chapter 2.

During indexing, stemming was applied to the documents and queries respectively, using the Krovetz stemmer (Krovetz, 1993). All documents were preprocessed using the dedicated preprocessing of each dataset. Specifically for BIOASQ the *bioclean* function was modified so that text is also split on dashes (-) which proved useful at least for the BM25 retrieval mostly because it provided higher recall, a measure essential to reranking. During searching, queries were preprocessed and stop-words were removed based on a dedicated list of stop-words for each dataset. This retrieval setup will be referred as BM25-SE.

3.3.2 Document reranking with neural networks

Training examples In order to use a dataset to train a neural network model, we will generate training pairs of a relevant and a non-relevant document for a query. For a query q let D_{rel} be the set of documents marked as relevant by humans. First, we retrieve the top N documents using BM25-SE which constitute a set of documents D_{ret}. Let D_{relRet} be the set of retrieved documents that are annotated as relevant:

$$D_{relRet} = D_{rel} \cap D_{ret} \tag{3.11}$$

Similarly, let $D_{nonRelRet}$ be the set of retrieved documents that are not marked as relevant:

$$D_{nonRelRet} = D_{ret} - D_{rel} \tag{3.12}$$

For each document d^+ in D_{relRet} we randomly sample a document d^- from $D_{nonrelRet}$ and then produce a training example (q, d^+, d^-), i.e. a query, a relevant document and a non-relevant document. The number of training examples produced by this query q will be equal to the size of D_{relRet} set. After repeating this process for every query in the training set, we obtain all the examples that we will use for the training of the neural networks. Early experiments indicated that using relevant documents not returned in the top N documents as positive documents to produce more training examples, leads to worse results. Moreover, using only the retrieved relevant documents makes it straightforward to use the BM25 score already calculated by BM25-SE, as input to the deep relevance matching models.

The number of documents retrieved with BM25-SE and used for training and re-ranking was set to $N = 100$ for the BIOASQ dataset and $N = 1000$ for the ROBUST 2004 dataset, numbers that provided a lot of room for reranking improvement (see Section 3.4) while keeping the number of documents to score low. Table 3.10 shows the number of training examples produced after the process described above, using the top N documents, as defined above for each dataset.

[11] The Galago search engine: https://www.lemurproject.org/galago.php (v. 3.10)

Dataset	#Training examples
BIOASQ	11,590
+EN-DE-EN	22,282
+EN-JA-EN	20,554
+EN-JA-DE-EN	20,148
ROBUST 2004	$5,934 \pm 201$

TABLE 3.10: Number of training examples produced per dataset. For BIOASQ, the number of training examples produced by data augmentation is also reported. For TREC ROBUST 2004, the average ($\pm$st.dev) of training examples over the five folds is reported.

Early stopping Each model was trained for M epochs and only the model's state achieving the best development performance (best epoch) is kept and used for the evaluation of the model on the test set. M was set to 100 for BIOASQ and 50 for TREC ROBUST 2004.

Training of word embeddings For the training of the word embeddings we used WORD2VEC (Mikolov et al., 2013). More specifically, we used the WORD2VEC implementation of the *gensim* Python toolkit[12] using the skip-gram model with a window of 5 words before and 5 words after the central word, negative sampling and embedding dimensions $r = 200$. Also, minimum corpus frequency was set to 5. All other parameters were set to the default values of *gensim*.

Model implementations The DRMM model was implemented using DyNet[13] in Python. For the PACRR based models we used and modified the Keras[14] implementation released by the authors (Hui et al., 2017; Hui et al., 2018)[15]. PACRR models where also implemented in DyNet providing similar results. Hyperparameters where chosen based on development evaluation. All models used a learning rate of 0.001 and $\beta_1/\beta_2 = 0.9/0.999$ with batch size equal to 32 and Glorot initialization (Glorot and Bengio, 2010).

Regarding DRMM, histogram size was set to 30, following Guo et al., 2016. Each histogram then goes through a 2-layer MLP with RELU activations and hidden layers with 10 dimensions to score the query term matching histogram.

For PACRR and TERM-PACRR, maximum query length l_q was set to 30 for BIOASQ and 5 for ROBUST 2004. Maximum document length l_d was set to 300 and 1000 for the two datasets, covering 92% and 90% of the documents of each dataset repsectively. Maximum kernel size $(l_g \times l_g)$ was set to (3×3) with number of filters per size $n_f = 16$. Row-wise k-max pooling used $k = 2$.

PACRR used a 2-layer MLP with RELU activations and hidden layers with 50 dimensions to score the document-aware query representation, while TERM-PACRR used a 2-layer MLP with RELU activations and hidden layers with 7 dimensions to independently score each document-aware query-term encoding.

[12] https://radimrehurek.com/gensim/models/word2vec.html (v. 3.3.0)
[13] The DyNet neural network toolkit: http://dynet.io/
[14] The Keras neural network toolkit: https://keras.io/
[15] Implementation of PACRR by Hui et al., 2017; Hui et al., 2018: https://github.com/khui/copacrr

Evaluation The BIOASQ measures were calculated using BIOASQ's official evaluation script[16] and the TREC ROBUST 2004 measures using the *trec_eval* tool[17].

3.4 Ideal reranking

As *oracle* we will refer to a reranking system that can always place the relevant documents on the top positions of the retrieved list of documents by having access to the relevance judgments of each query. Similarly to the neural re-ranking methods, we will apply *oracle* to the list of documents retrieved by BM25-SE, in order to find out the best possible performance that a reranking system can achieve (ideal reranking). It is easily perceived that the *oracle*'s performance is strongly associated with the number of relevant documents found in the retrieved list, that is the recall of BM25-SE.

3.5 Experimental results

This section presents the experimental results of the systems described, on BIOASQ6 and TREC ROBUST 2004 datasets. All reported results are the average of five different runs (five random initializations) with standard deviation shown for each model (unless otherwise stated).

3.5.1 BioASQ experiments

First we are going to evaluate the methods on BIOASQ6-DEV and then on BIOASQ6-TEST to examine the consistency of each system's performance. Finally, we present the results of our participation in the document retrieval task of the 6^{th} year of BIOASQ (Task6b-phase A) that took place during March to May 2018.

Table 3.11 reports the performance of the methods in the BIOASQ6-DEV set. System ranking is based on $MAP^{\star}$. We can see that BM25 outperforms both PACRR and TERM-PACRR models with the latter performing significantly better than the former. Also, PACRR-RNN performs worse and is less consistent than its revised model, PACRR. DRMM performs slightly better than BM25 and outperforms the other PACRR based methods, when external features are not used. After the addition of the BM25 and overlap features to the deep relevance ranking models, all three models are significantly improved and outperform BM25 by a larger margin. Among the three models using the extra features, TERM-PACRR-EXTRA is the best performing model on BIOASQ6-DEV data. Finally, we can observe that the *oracle*'s performance is quite high which indicates the reranking performance is not capped and can be improved further.

[16]The oficcial evaluation script of BIOASQ: https://github.com/BioASQ/Evaluation-Measures
[17]The trec_eval tool for ad-hoc IR evaluation: https://trec.nist.gov/trec_eval/ (v. 9.0)

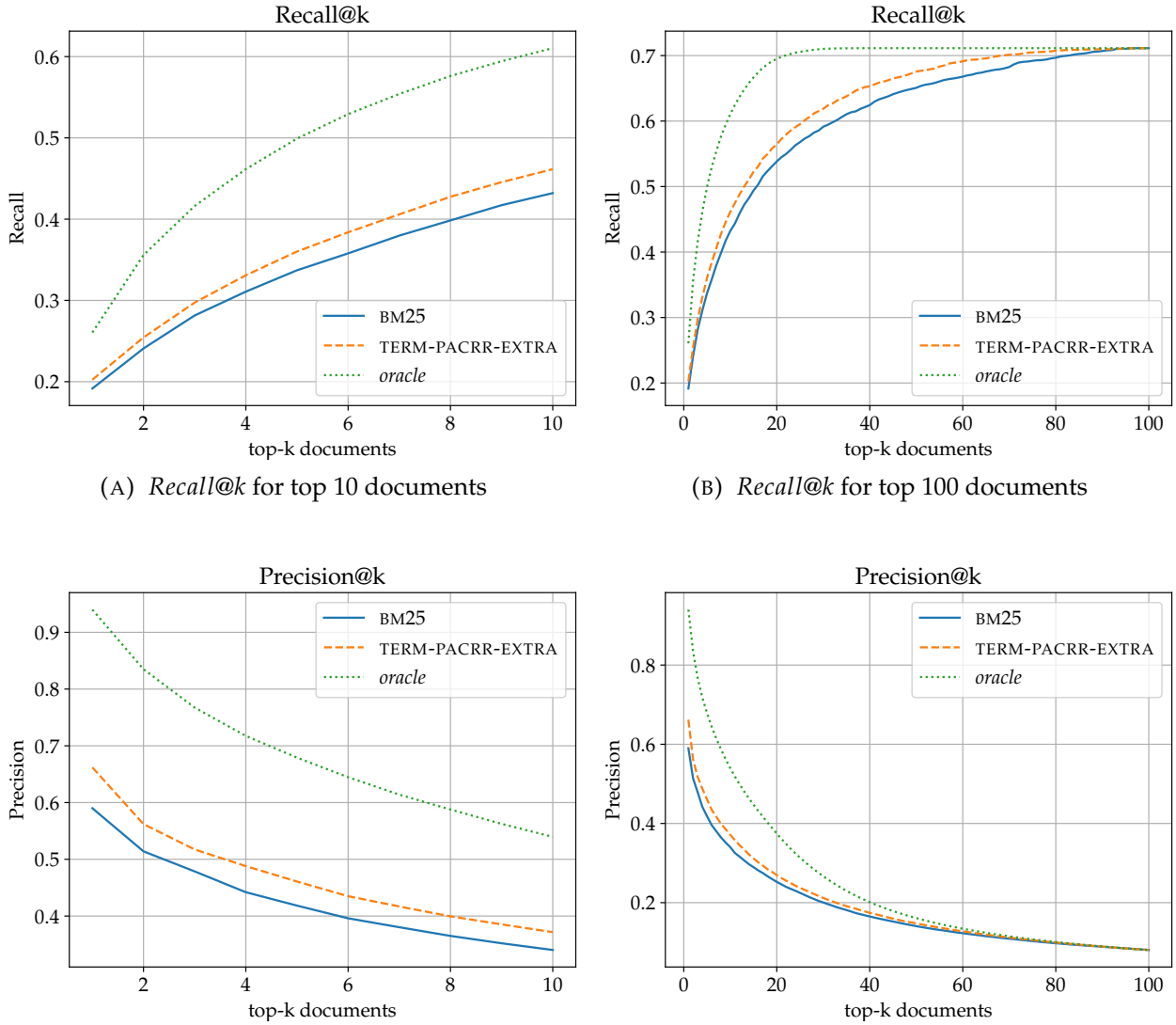
System	*MAP⋆*	*GMAP*	*Precision*	*Recall*	*F-measure*
Traditional IR Baseline					
BM25	27.4 ± 0.0	4.6 ± 0.0	35.2 ± 0.0	43.2 ± 0.0	29.8 ± 0.0
Deep relevance ranking					
DRMM	27.8 ± 0.7	4.6 ± 0.3	35.6 ± 0.5	43.2 ± 0.5	30.3 ± 0.4
PACRR-RNN	23.6 ± 1.3	3.5 ± 0.6	31.9 ± 0.9	41.1 ± 1.2	27.6 ± 0.8
PACRR	24.2 ± 0.3	3.3 ± 0.3	32.2 ± 0.3	40.8 ± 0.6	27.7 ± 0.3
TERM-PACRR	26.8 ± 0.3	4.9 ± 0.4	34.6 ± 0.4	43.9 ± 0.6	29.9 ± 0.4
Deep relevance ranking with extra features					
DRMM-EXTRA	30.4 ± 0.2	5.8 ± 0.1	37.6 ± 0.2	45.6 ± 0.3	31.9 ± 0.2
PACRR-EXTRA	30.4 ± 0.1	5.6 ± 0.2	37.7 ± 0.1	45.5 ± 0.2	31.9 ± 0.1
TERM-PACRR-EXTRA	$\mathbf{31.0 \pm 0.2}$	$\mathbf{6.1 \pm 0.2}$	$\mathbf{38.2 \pm 0.1}$	$\mathbf{46.2 \pm 0.1}$	$\mathbf{32.4 \pm 0.1}$
oracle	54.5 ± 0.0	22.0 ± 0.0	61.8 ± 0.0	70.9 ± 0.0	54.5 ± 0.0

TABLE 3.11: Performance on BIOASQ6-DEV.

In Table 3.12 we investigate how the BM25 and overlap features affect the performance of the systems when added separately as well as when used together as input to the models. We can see that both BM25 and overlap features improve the performance of all three systems. When added on its own, BM25 improves the performance of the systems by a larger margin than overlap features do. When all features are used together (EXTRA), all three models achieve the best performance. We will use this conclusion to report further results only for models that use all extra features.

System	*MAP⋆*	*GMAP*	*Precision*	*Recall*	*F-measure*
DRMM					
DRMM	$27.8 \pm .7$	$4.6 \pm .3$	$35.6 \pm .5$	$43.2 \pm .5$	$30.3 \pm .4$
DRMM-BM25	$30.2 \pm .2$	$5.4 \pm .2$	$37.5 \pm .2$	$45.2 \pm .2$	$31.6 \pm .2$
DRMM-OL	$28.4 \pm .3$	$5.3 \pm .2$	$36.1 \pm .3$	$44.5 \pm .3$	$30.8 \pm .2$
DRMM-EXTRA	$\mathbf{30.4 \pm .2}$	$\mathbf{5.8 \pm .1}$	$\mathbf{37.6 \pm .2}$	$\mathbf{45.6 \pm .3}$	$\mathbf{31.9 \pm .2}$
PACRR					
PACRR	$24.2 \pm .3$	$3.3 \pm .3$	$32.2 \pm .3$	$40.8 \pm .6$	$27.7 \pm .3$
PACRR-BM25	$29.7 \pm .2$	$5.6 \pm .1$	$37.1 \pm .1$	$44.9 \pm .2$	$31.4 \pm .1$
PACRR-OL	$26.4 \pm .3$	$4.2 \pm .2$	$34.2 \pm .4$	$42.9 \pm .3$	$29.3 \pm .3$
PACRR-EXTRA	$\mathbf{30.4 \pm .1}$	$\mathbf{5.6 \pm .2}$	$\mathbf{37.7 \pm .1}$	$\mathbf{45.5 \pm .2}$	$\mathbf{31.9 \pm .1}$
TERM-PACRR					
TERM-PACRR	$26.8 \pm .3$	$4.9 \pm .4$	$34.6 \pm .4$	$43.9 \pm .6$	$29.9 \pm .4$
TERM-PACRR-BM25	$30.5 \pm .1$	$6.1 \pm .1$	$37.8 \pm .2$	$45.8 \pm .3$	$32.1 \pm .2$
TERM-PACRR-OL	$27.9 \pm .4$	$5.3 \pm .2$	$35.8 \pm .3$	$44.7 \pm .3$	$30.7 \pm .2$
TERM-PACRR-EXTRA	$\mathbf{31.0 \pm .2}$	$\mathbf{6.1 \pm .2}$	$\mathbf{38.2 \pm .1}$	$\mathbf{46.2 \pm .1}$	$\mathbf{32.4 \pm .1}$

TABLE 3.12: Performance contribution of the extra features, on BIOASQ6-DEV.



(A) *Recall@k* for top 10 documents

(B) *Recall@k* for top 100 documents

(C) *Precision@k* for top 10 documents

(D) *Precision@k* for top 100 documents

FIGURE 3.4: Precision@k and Recall@k curves of TERM-PACRR-EXTRA against the BM25 baseline and the *oracle*, for top 10 and top 100 documents, on BIOASQ6-DEV.

System	top 10		top 100	
	AUP@k	*AUR@k*	*AUP@k*	*AUR@k*
BM25	42.77	33.47	17.93	60.94
TERM-PACRR-EXTRA	46.98	35.69	19.02	62.89
oracle	68.87	48.57	24.17	68.36

TABLE 3.13: Area under precision@k (*AUP@k*) and area under recall@k (*AUR@k*), on BIOASQ6-DEV.

Figure 3.4 shows the *Precision@k* and *Recall@k* curves discussed in Section 3.2, for the model with the best performance, TERM-PACRR-EXTRA (for a single run). We are mainly interested in the *Recall@k* curves and we can observe that the distinction between TERM-PACRR-EXTRA and BM25 is clearer than in the *Precision@k* curve, at least for top 100 documents. The approximated area under those curves is shown in Table 3.13.

Table 3.14 reports the results on BIOASQ6-TEST using $MAP^{\star}$. (For detailed results see Appendix A). The ranking and relative performance differences of the models are similar to those in BIOASQ6-DEV with some small diversions. PACRR-RNN performs slightly better than PACRR in batches 1, 3 and 5, but again is less consistent (larger std. dev.) than the other models. Also DRMM is slightly worse than BM25 for batches 1 and 5 but it performs better on the other 3 batches. TERM-PACRR-EXTRA is the best model in all 5 batches, followed by PACRR-EXTRA and DRMM-EXTRA. The scores achieved by the systems are significantly lower than those reported on BIOASQ6-DEV. The reason behind this is that each query has a very limited number of annotated documents since, by the time of writing, experts have not augmented them with additional relevant documents found during human evaluation (which has happened in BIOASQ6-DEV).

System	BATCH-1	BATCH-2	BATCH-3	BATCH-4	BATCH-5
Traditional IR Baseline					
BM25	10.8 ± .0	09.1 ± .0	09.1 ± .0	08.4 ± .0	05.4 ± .0
Deep relevance ranking					
DRMM	10.7 ± .2	09.5 ± .2	09.9 ± .3	08.9 ± .1	05.2 ± .2
PACRR-RNN	09.1 ± .7	09.0 ± .8	08.7 ± .7	07.7 ± .8	04.8 ± .6
PACRR	08.9 ± .5	09.3 ± .2	08.4 ± .4	07.9 ± .4	04.6 ± .2
TERM-PACRR	10.5 ± .3	10.4 ± .4	09.9 ± .4	08.5 ± .2	05.4 ± .3
Deep relevance ranking with extra features					
DRMM-EXTRA	11.7 ± .2	10.9 ± .2	11.1 ± .1	09.4 ± .1	06.0 ± .1
PACRR-EXTRA	11.8 ± .1	10.9 ± .1	11.0 ± .1	09.3 ± .0	06.0 ± .1
TERM-PACRR-EXTRA	**12.2 ± .2**	**11.2 ± .2**	**11.0 ± .2**	**09.4 ± .1**	**06.3 ± .2**
oracle	31.2 ± .0	27.0 ± .0	25.7 ± .0	22.4 ± .0	20.8 ± .0

TABLE 3.14: Performance ($MAP^{\star}$) on BIOASQ6-TEST-[1-5] batches.

Data augmentation experiments

In this section we will examine the results of data augmentation using translation as described in Section 3.1.1, applied to the training data of the two best performing models on development: DRMM-EXTRA and TERM-PACRR-EXTRA. We can see that the TERM-PACRR-EXTRA model did not benefit from the additional training examples, as training with augmented data provided slightly worse results than just using the original data. The DRMM-EXTRA model is slightly improved when using EN-DE-EN and EN-JA-DE-EN, however this improvement is probably not significant given the larger number of training examples. Overall, augmenting the queries with translation did not provide significant improvements to the models. One possible explanation is that important scientific terms, which appear very often in the biomedical queries of BIOASQ, usually remain the same during translation to another language and back, so only simple, low importance words or phrases change. These changes might not suffice to augment scientific text.

System	*MAP**	*GMAP*	*Precision*	*Recall*	*F-measure*
DRMM-EXTRA	$30.4 \pm .2$	$5.8 \pm .1$	$37.6 \pm .2$	$45.6 \pm .3$	$31.9 \pm .2$
+EN-DE-EN	$30.6 \pm .3$	$5.7 \pm .2$	$37.8 \pm .2$	$45.7 \pm .2$	$32.0 \pm .1$
+EN-JA-EN	$30.4 \pm .2$	$5.8 \pm .2$	$37.7 \pm .2$	$45.5 \pm .2$	$31.9 \pm .2$
+EN-JA-DE-EN	$30.5 \pm .1$	$5.7 \pm .3$	$37.8 \pm .2$	$45.6 \pm .3$	$32.0 \pm .2$
TERM-PACRR-EXTRA	$31.0 \pm .2$	$6.1 \pm .2$	$38.2 \pm .1$	$46.2 \pm .1$	$32.4 \pm .1$
+EN-DE-EN	$30.6 \pm .3$	$6.0 \pm .2$	$37.9 \pm .3$	$46.0 \pm .1$	$32.2 \pm .2$
+EN-JA-EN	$30.7 \pm .3$	$6.0 \pm .1$	$38.1 \pm .2$	$46.2 \pm .1$	$32.3 \pm .1$
+EN-JA-DE-EN	$30.7 \pm .2$	$6.0 \pm .1$	$38.1 \pm .2$	$46.2 \pm .2$	$32.3 \pm .2$

TABLE 3.15: Performance of DRMM-EXTRA and TERM-PACRR-EXTRA on BIOASQ6-DEV, using the original training data vs. augmented via 3 translation strategies.

Participation in BIOASQ Task6b-phase A

In this section we present the performance of TERM-PACRR-EXTRA after participating in the BIOASQ Task6b-phase A challenge for document ranking. For the training of the model we used BIOASQ6-TRAIN augmented by an additional 400 queries from the BIOASQ6-DEV set. A small development set of the remaining 100 queries of BIOASQ6-DEV was still used for epoch selection. In order to moderate the fluctuations in performance due to the random initialization of the network parameters, we trained 10 different instances of the model and for each test query the predicted document ranking was based on the following voting scheme: Each instance of the model votes for a document with $11 - i$ points where $i = 1, 2, \ldots, 10$ is the position where this document was ranked by this instance. Then the points of each document from the 10 instances are aggregated to produce the final ranking.

We used TERM-PACRR-EXTRA under the name *aueb-nlp-1*. Below we provide a brief description of the rest *aueb-nlp-[2-4]* systems that we submitted, as part of the AUEB entry. For further information on *aueb-nlp-[2-4]*, consult Brokos et al., 2018.

- *aueb-nlp-2*: A DRMM-EXTRA based model using context aware term representations, instead of fixed pre-trained embeddings, and document-aware query-term representations produced by an attention (over document terms) mechanism, instead of the matching histograms.
- *aueb-nlp-3*: A ensemble of TERM-PACRR-EXTRA with *aueb-nlp-2*.
- *aueb-nlp-4*: A model based on *aueb-nlp-2* that also produces scores for windows over of the document in order to reward relevance matching if found in a dense window.
- *aueb-nlp-5*: The *aueb-nlp-4* system modified to increase precision over recall, which proved beneficial for our participation in the snippet extraction task of BIOASQ.

At this point we should make clear that the previously reported experiments (Table 3.14) use the same test set that the competition uses, but those (previous reported) experiments took place after the completion of the competition, when the gold answers and documents were

released. By contrast, Table 3.16 shows the performance and ranking position of TERM-PACRR-EXTRA on each test batch, in comparison with the winning system, reporting results before the manual evaluation by humans, since this process was not completed at the time of writing, thus these are not final. The first thing to observe is that TERM-PACRR-EXTRA's performance is in line with the already reported experiments. TERM-PACRR-EXTRA does not achieve the best performance on any batch, however for batches 1, 4 and 5 it is in the top 5 systems. Moreover, the performance difference from the winning systems is small with the exception of batch 3, where TERM-PACRR-EXTRA is worse than the winning system by a large margin in terms of *MAP** and *Recall*, however achieves better *Precision* and *F-measure*. Another interesting observation is that the winning systems in 4 out of 5 batches are *aueb-nlp* systems which, as already mentioned, are deep learning systems based on TERM-PACRR-EXTRA and DRMM-EXTRA.

System	Ranking	*MAP**	*GMAP*	*Precision*	*Recall*	*F-measure*
Batch1						
aueb-nlp-3	1/14	**12.71**	2.80	**19.15**	**59.70**	**25.64**
TERM-PACRR-EXTRA	3/14	12.46	**2.82**	19.05	59.09	25.46
Batch2						
aueb-nlp-2	1/21	**12.07**	**2.00**	**18.30**	**61.30**	**24.73**
TERM-PACRR-EXTRA	9/21	10.96	1.48	16.50	58.55	22.64
Batch3						
ustb_prir2	1/23	**12.81**	**1.13**	16.60	**56.74**	21.86
TERM-PACRR-EXTRA	9/23	11.22	1.01	**18.77**	53.99	**23.45**
Batch4						
aueb-nlp-3	1/20	**10.00**	0.68	15.56	55.67	21.34
TERM-PACRR-EXTRA	4/20	09.71	**0.70**	15.56	**56.37**	**21.36**
Batch5						
aueb-nlp-4	1/22	**6.95**	**0.12**	**11.45**	**37.90**	**15.90**
TERM-PACRR-EXTRA	5/22	6.46	0.09	11.05	35.96	14.41

TABLE 3.16: BIOASQ Task6b-phase A results for TERM-PACRR-EXTRA and the winning system per test batch.

3.5.2 TREC Robust 2004 experiments

The systems were also evaluated on the data from the TREC ROBUST 2004 ad-hoc retrieval task. Table 3.17 reports their performance in the development data, including the BM25 baseline and the *oracle*. The results are in line with those on the BIOASQ dataset with a few deviations. DRMM outperforms PACRR and TERM-PACRR, and it is slightly better than the BM25 baseline. After adding the extra features, all three models are improved and outperform BM25 by a large margin. Unlike the BIOASQ experiments, here the best model is DRMM-EXTRA (instead of TERM-PACRR-EXTRA).

System	*MAP*	*Precision*@20	*nDCG*@20
Traditional IR Baseline			
BM25	23.8 ± 0.0	35.4 ± 0.0	42.5 ± 0.0
Deep relevance ranking			
DRMM	23.9 ± 0.8	34.0 ± 1.0	40.9 ± 1.4
PACRR	21.2 ± 0.4	31.9 ± 0.9	38.3 ± 0.8
TERM-PACRR	21.5 ± 0.6	31.7 ± 1.5	38.3 ± 1.5
Deep relevance ranking with extra features			
DRMM-EXTRA	$\mathbf{26.2 \pm 0.7}$	$\mathbf{37.0 \pm 1.2}$	$\mathbf{44.3 \pm 1.5}$
PACRR-EXTRA	25.9 ± 0.2	37.3 ± 0.4	44.5 ± 0.4
TERM-PACRR-EXTRA	26.0 ± 0.3	37.5 ± 0.6	44.8 ± 0.7
oracle	68.0 ± 0.0	82.1 ± 0.0	93.1 ± 0.0

TABLE 3.17: Performance on the TREC ROBUST 2004 development data.

The last thing to notice is that the *oracle*'s performance is quite high which means that the reranking can be improved further.

The systems' performance on the test data is reported in Table 3.18. We can see that the conclusions are similar to those reached by the evaluation on the development set. A difference is that DRMM is now slightly worse than BM25. Also, TERM-PACRR-EXTRA achieves the same and more consistent (smaller std. dev) $MAP^\star$ score compared to DRMM-EXTRA and is slightly better in the other measures. Notice that BM25 and *oracle* performance is the same in both development and test since these are calculated with macro-averaging along the same 5 splits.

System	*MAP*	*Precision*@20	*nDCG*@20
Traditional IR Baseline			
BM25	23.8 ± 0.0	35.4 ± 0.0	42.5 ± 0.0
Deep relevance ranking			
DRMM	23.6 ± 0.6	33.5 ± 0.9	40.2 ± 1.0
PACRR	21.0 ± 0.5	31.5 ± 0.6	38.0 ± 0.8
TERM-PACRR	21.1 ± 0.7	31.9 ± 1.5	38.2 ± 1.6
Deep relevance ranking with extra features			
DRMM-EXTRA	$\mathbf{25.8 \pm 0.8}$	36.9 ± 1.2	43.9 ± 1.3
PACRR-EXTRA	25.7 ± 0.3	37.1 ± 0.3	44.2 ± 0.5
TERM-PACRR-EXTRA	$\mathbf{25.8 \pm 0.4}$	$\mathbf{37.2 \pm 0.7}$	$\mathbf{44.3 \pm 0.8}$
oracle	68.0 ± 0.0	82.1 ± 0.0	93.1 ± 0.0

TABLE 3.18: Performance on the TREC ROBUST 2004 test data.

Chapter 4

Related Work

Document relevance ranking is a standard problem in information retrieval, widely studied over the years. Traditional approaches consist of term weighting schemes (Robertson and Jones, 1988), and methods based on statistical NLP like the query likelihood model (Ponte and Croft, 1998) that scores each document by the probability assigned to a query by the statistical language model of the document. Another method, extensively used and described in this thesis, that is derived from probabilistic methods of relevance ranking is BM25 (Robertson and Zaragoza, 2009).

The recent outbreak of deep learning has lead to state-of-the-art results in various NLP tasks, influencing the research in deep learning for document relevance ranking (Zhang et al., 2016; Onal et al., 2017; Craswell et al., 2018). One of the first successful works is the DSSM model of Huang et al., 2013. DSSM first hashes a query or a document, in sparse vectors that indicate the n-grams contained in its text, similarly to term level sparse vectors that are widely used in conventional IR to represent documents, but using significantly fewer dimensions. These hashed query and document representations are then passed through multiple non-linear layers to produce high level, low dimensional representations for a query and each candidate document. Then, cosine similarity between the query and each document representation is used as the documents' relevance scores. The model is trained using click-through data, by maximizing the likelihood (relevance score) of the clicked documents given the query.

An extension of this model is CLSM (or CDSSM) of Shen et al., 2014, which applies convolution to the hashed term representations to obtain contextual information and then applies max pooling to aggregate the output of each convolution into a vector that represents a query or document. This vector is then passed though a single non-linear layer to produce the final high level representation.

The advent of large-scale word embeddings (Mikolov et al., 2013; Pennington et al., 2014), opened the way for new relevance ranking models that utilize these rich term representations instead of the conventional sparse vectors. Two of these models is the DRMM model of Guo et al., 2016 and the PACRR model of Hui et al., 2017 that were analyzed and used in this thesis. Another model is K-NRM of Xiong et al., 2017 which first calculates a translation matrix containing word to word similarities or word embeddings (similar to PACRR's similarity matrix) and then applies multiple (k) kernels to each row, to produce a document dependent representation (k-dimensional) for each query term. Then the representations of all query terms are aggregated through logarithm of their summation and the resulting query-document representation

passes through a non-linear layer to produce the relevance score. The model is trained using hinge loss on pairs of relevant and non-relevant documents, given a query.

A different approach to the widely used query-document interaction matrix is that of Jaech et al., 2017. First, the word embeddings of a query q and a document d pass through separate bidirectional LSTMs. A linear projection matrix is applied to the hidden states of both BI-LSTMs, to obtain term representations with the same dimensionality k. In contrast to PACRR, K-NRM and other works, Jaech et al., 2017 use element-wise (Hadamard) product between each query and each document term vector resulting in a $(|q| \times |d| \times k)$ 3-*D Match-Tensor*. An extra dimension is added $(k+1)$ containing binary exact matching signals. Subsequently, multiple 3-*D* convolutions are applied to the matching tensor and the outputs of max pooling for each of those are aggregated into a final query-document representation vector that is passed through a fully-connected layer to produce a relevance score.

The main evaluation in this thesis utilized data of the biomedical domain. A related work on biomedical IR using deep learning is this of Mohan et al., 2017. As a first stage, the proposed model computes simple interactions between each document term and its closest, in terms of Euclidean distance, query term. After applying convolution to these interactions and max pooling, the resulting document-query representation is combined with overlap features similar to those used in this thesis. The combined vector then passes through an MLP to produce a relevance score. An important distinction of this work with ours is that it utilizes click-though data from PubMed, instead of a relatively small training dataset like the one we used from BIOASQ.

Chapter 5

Conclusions and future work

5.1 Conclusions

In this thesis, we explored the use of deep neural networks for document relevance reranking in IR. In particular, we experimented with two models (DRMM and PACRR) that have been shown to outperform strong traditional IR baselines like BM25. We applied these methods on two different datasets; the BIOASQ dataset and and the widely used in IR, TREC ROBUST 2004 dataset. Moreover, we proposed various modifications in order to improve the performance of the models. These include changes in PACRR's architecture (TERM-PACRR) and the integration of additional features to all models, in order to capture strong exact matching signals, critical to IR tasks. As a first step in data augmentation, we experimented with additional data produced by translating queries to another language and back, showing that models did not significantly benefit. Finally, we reported the results of our participation in the 6^{th} BIOASQ challenge as AUEB, using the best performing model of this thesis (TERM-PACRR-EXTRA) which achieved competitive performance, often exceeded only by deep learning methods relevant to those we used, also submitted by our AUEB team. To conclude, we saw that the success of deep learning in various NLP tasks has inspired its use in the document relevance ranking field of IR, with significant performance gains over traditional well-established methods.

5.2 Future Work

A simple extension of this work could be the replacement of WORD2VEC embeddings with FASTTEXT embeddings (Bojanowski et al., 2017), that have been shown to perform better in some NLP tasks.

An important limitation of the reported experiments was the size of the datasets. Deep learning methods usually utilize hundreds of thousands or even millions of training examples, whereas the BIOASQ dataset provides only a few thousands and TREC ROBUST 2004 even fewer. Experimenting with augmentation via translation did not provide the desired results, however more sophisticated data augmentation techniques could be considered in future works (DeVries and Taylor, 2017). A factor that could significantly improve the performance of the models is the use of click-though user data, as happens with large corporations (Joachims, 2002; Mohan et al., 2017). However access to this kind of data is usually difficult due to privacy issues.

Finally, the models used in this thesis belong to the interaction-focused category, which makes it difficult to index documents and perform full document retrieval. Representation-focused models that use attention mechanisms (Bahdanau et al., 2015) could be considered in order to both capture strong exact or near matching signals and make it possible to produce query independent document representations that can be indexed and retrieved during search time, without having to use a reranking strategy.

Appendix A

Tables A.1, A.2, A.3, A.4 and A.5, report detailed results of the methods evaluation in each batch of the BIOASQ6-TEST data.

System	*MAP**	*GMAP*	*Precision*	*Recall*	*F-measure*
Traditional IR Baseline					
BM25	10.8 ± 0.0	1.9 ± 0.0	17.2 ± 0.0	55.9 ± 0.0	23.2 ± 0.0
Deep relevance ranking					
DRMM	10.7 ± 0.0	2.0 ± 0.2	17.1 ± 0.1	53.9 ± 0.4	23.0 ± 0.1
PACRR-RNN	09.1 ± 0.7	1.0 ± 0.3	15.0 ± 0.9	49.5 ± 2.2	20.2 ± 1.1
PACRR	08.9 ± 0.5	1.1 ± 0.1	14.8 ± 0.4	49.8 ± 0.7	20.1 ± 0.5
TERM-PACRR	10.5 ± 0.3	1.6 ± 0.2	16.8 ± 0.3	53.8 ± 0.7	22.6 ± 0.4
Deep relevance ranking with extra features					
DRMM-EXTRA	11.7 ± 0.2	2.3 ± 0.4	18.3 ± 0.4	58.1 ± 0.9	24.6 ± 0.5
PACRR-EXTRA	11.8 ± 0.1	2.1 ± 0.2	18.0 ± 0.2	56.6 ± 0.5	24.0 ± 0.2
TERM-PACRR-EXTRA	12.2 ± 0.2	2.3 ± 0.1	18.5 ± 0.4	57.8 ± 0.6	24.8 ± 0.4
oracle	31.2 ± 0.0	16.2 ± 0.0	96.0 ± 0.0	86.8 ± 0.0	31.2 ± 0.0

TABLE A.1: Performance on BIOASQ6-TEST-BATCH-1.

System	*MAP**	*GMAP*	*Precision*	*Recall*	*F-measure*
Traditional IR Baseline					
BM25	09.1 ± 0.0	0.7 ± 0.0	14.3 ± 0.0	50.0 ± 0.0	19.4 ± 0.0
Deep relevance ranking					
DRMM	09.5 ± 0.2	0.8 ± 0.1	15.0 ± 0.4	52.8 ± 1.5	20.4 ± 0.5
PACRR-RNN	09.0 ± 0.8	0.8 ± 0.2	14.4 ± 0.7	51.3 ± 2.5	19.7 ± 1.0
PACRR	09.3 ± 0.2	0.9 ± 0.1	14.9 ± 0.1	52.7 ± 1.1	20.3 ± 0.1
TERM-PACRR	10.4 ± 0.4	1.4 ± 0.2	15.9 ± 0.5	56.0 ± 1.6	21.6 ± 0.7
Deep relevance ranking with extra features					
DRMM-EXTRA	10.9 ± 0.2	1.5 ± 0.1	16.8 ± 0.3	58.3 ± 0.5	22.8 ± 0.4
PACRR-EXTRA	10.9 ± 0.1	1.6 ± 0.1	16.6 ± 0.2	58.3 ± 0.4	22.7 ± 0.2
TERM-PACRR-EXTRA	11.2 ± 0.2	1.7 ± 0.2	16.8 ± 0.2	59.4 ± 0.4	23.0 ± 0.2
oracle	27.0 ± 0.0	10.7 ± 0.0	93.0 ± 0.0	78.5 ± 0.0	83.0 ± 0.0

TABLE A.2: Performance on BIOASQ6-TEST-BATCH-2.

System	*MAP**	*GMAP*	*Precision*	*Recall*	*F-measure*
Traditional IR Baseline					
BM25	09.1 ± 0.0	0.5 ± 0.0	15.8 ± 0.0	49.0 ± .0	20.1 ± .0
Deep relevance ranking					
DRMM	09.9 ± 0.3	0.6 ± 0.1	17.8 ± 0.3	50.9 ± 0.6	22.3 ± 0.3
PACRR-RNN	08.7 ± 0.7	0.5 ± 0.1	16.6 ± 0.6	47.7 ± 1.3	20.7 ± 0.6
PACRR	08.4 ± 0.4	0.5 ± 0.1	16.5 ± 0.5	47.8 ± 1.3	20.6 ± 0.6
TERM-PACRR	09.9 ± 0.4	0.7 ± 0.1	17.7 ± 0.5	50.6 ± 1.3	22.2 ± 0.6
Deep relevance ranking with extra features					
DRMM-EXTRA	11.1 ± 0.1	1.0 ± 0.1	18.7 ± 0.3	54.1 ± 0.5	23.5 ± 0.3
PACRR-EXTRA	11.0 ± 0.1	1.0 ± 0.1	18.6 ± 0.1	53.3 ± 0.4	23.2 ± 0.2
TERM-PACRR-EXTRA	11.0 ± 0.2	1.0 ± 0.1	18.6 ± 0.3	53.7 ± 0.7	23.3 ± 0.3
oracle	25.7 ± 0.0	6.8 ± 0.0	89.0 ± 0.0	71.2 ± 0.0	76.7 ± 0.0

TABLE A.3: Performance on BIOASQ6-TEST-BATCH-3.

System	*MAP**	*GMAP*	*Precision*	*Recall*	*F-measure*
Traditional IR Baseline					
BM25	08.4 ± 0.0	0.5 ± 0.0	13.8 ± 0.0	52.0 ± 0.0	19.1 ± 0.0
Deep relevance ranking					
DRMM	08.9 ± 0.1	0.4 ± 0.0	14.9 ± 0.2	51.3 ± 0.8	20.2 ± 0.3
PACRR-RNN	07.7 ± 0.8	0.3 ± 0.1	13.1 ± 1.0	47.3 ± 2.9	18.1 ± 1.3
PACRR	07.9 ± 0.4	0.3 ± 0.1	13.2 ± 0.4	47.9 ± 0.2	18.3 ± 0.5
TERM-PACRR	08.5 ± 0.2	0.5 ± 0.1	14.1 ± 0.2	51.5 ± 0.7	19.5 ± 0.3
Deep relevance ranking with extra features					
DRMM-EXTRA	09.4 ± 0.1	0.6 ± 0.0	15.1 ± 0.1	54.9 ± 0.7	20.8 ± 0.1
PACRR-EXTRA	09.3 ± 0.0	0.6 ± 0.0	15.3 ± 0.2	55.4 ± 0.8	21.1 ± 0.3
TERM-PACRR-EXTRA	09.4 ± 0.1	0.7 ± 0.0	15.3 ± 0.2	56.1 ± 0.8	21.1 ± 0.2
oracle	22.4 ± 0.0	3.3 ± 0.0	82.0 ± 0.0	72.2 ± 0.0	75.1 ± 0.0

TABLE A.4: Performance on BIOASQ6-TEST-BATCH-4.

System	*MAP**	*GMAP*	*Precision*	*Recall*	*F-measure*
Traditional IR Baseline					
BM25	05.4 ± 0.0	0.5 ± 0.0	09.2 ± 0.0	28.6 ± 0.0	12.8 ± .00
Deep relevance ranking					
DRMM	05.2 ± 0.2	0.1 ± 0.0	09.4 ± 0.2	30.8 ± 0.4	13.2 ± 0.2
PACRR-RNN	04.8 ± 0.6	0.1 ± 0.0	08.8 ± 0.4	28.4 ± 1.0	12.2 ± 0.5
PACRR	04.6 ± 0.2	0.1 ± 0.0	08.8 ± 0.5	27.7 ± 2.1	12.2 ± 0.7
TERM-PACRR	05.4 ± 0.3	0.1 ± 0.0	09.8 ± 0.3	31.4 ± 1.1	13.6 ± 0.3
Deep relevance ranking with extra features					
DRMM-EXTRA	06.0 ± 0.1	0.1 ± 0.0	10.1 ± 0.4	33.7 ± 1.3	14.2 ± 0.5
PACRR-EXTRA	06.0 ± 0.1	0.1 ± 0.0	10.0 ± 0.2	34.1 ± 1.0	14.1 ± 0.3
TERM-PACRR-EXTRA	06.3 ± 0.2	0.1 ± 0.0	10.6 ± 0.1	35.3 ± 0.5	14.8 ± .02
oracle	20.8 ± 0.0	1.7 ± 0.0	75.0 ± 0.0	00.0 ± 0.0	61.8 ± .00

TABLE A.5: Performance on BIOASQ6-TEST-BATCH-5.

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