Reproducing experimental results from paper: Entity Set Search of Scientific Literature: An Unsupervised Ranking[1]

Reproducibility Report\*

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ABSTRACT

As newcomers, our ultimate goal is to primarily investigate the reproducibility of the – above referred – scientific paper; check the consistency of the outcome; validate its correctness and accuracy; and potentially challenge the ultimate conclusions by strictly following the original execution steps. The scope of the reproducing activity is defined as part of the Exercise 2 of the lecture “Experiment Design for Data Science” in 2021WS.

The hypothesis of the original experiment was to prove that the self-developed *SetRank*-algorithm, a novel unsupervised model selection approach, significantly outperforms the current web or general domain search approaches for searching scientific literatures. Especially regarding entity-set queries modelling inter-entity relations and capturing entity type information. For the experiment, two predefined sets of data were used.

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KEYWORDS

Entity-Set Aware Search; Unsupervised Ranking Model; Unsupervised Model Selection; Literature Search; …

ACM Reference format:

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1 Introduction

Nowadays, it is an elementary expectation from research papers to be documented in a way, that the underlying calculations and results contributing to the final conclusions are reproducible, based on documented workflows, accessible data and code basis. Here, we intend to describe the performed steps and the faced issues that we met in course of our reproducing experiment. In case of conceptual or technical gaps, we follow a conservative approach (to stay close to the anticipated, original process steps). As final step, we present the differences between the documented results and the re-calculated ones (including significance testing).

According to the original research paper, scientific literature search is different from Web or general domain search (working with short keyword queries). The majority of queries in scientific literature search are (concrete or abstract) *entity-set ones*. They reflect user’s need for finding documents that (i) contain multiple entities, (ii) reveal inter-entity relationships and (iii) the query provides a ranked list of documents that are most relevant to the whole entity set – in contrast to supervised approaches that model each entity separately (based on click history). *SetRank*, unsupervised ranking framework is developed to model inter-entity relationships and captures entity type information based on the technique of weighted rank aggregation. It first links entity mentions in query and documents to an external knowledgebase. Then, each document is represented with both *bag-of-words* and *bag-of-entities representations* and fits two language models respectively. A novel heterogeneous graph representation models complex entity information(e.g., entity type) and entity relations within the set. Then, the query-document matching is defined as a graph covering process and each document is ranked based on the information need it covers in the query graph. Some parameters still need to be learned using a labelled validation set.

The main conclusions are made, by reporting the implemented SetRank algorithm to four different, commonly used baseline models:

* BM25: Vector space model
* LM-DIR: Query likelihood model using Dirichlet Smoothing
* LM-JM: Query likelihood model using Jelinek Mercer Smoothing
* IB: Information-based model

Calculation are done for a biomedical genomics track(TREC-BIO) dataset, as well as for Semantic Scholar query data (S2-C2) covering the field of Computer Science.

The algorithms are then compared with the Normalized Discounted Cumulative Gain (NDCG), which is an adequate measure for the performance of recommender systems.

The remaining part of this report is organized as follows: In Section 2 related strategic approach for the reproducibility are discussed. Section 3 presents the faced difficulties over the experiments in connection to the execution process steps. Section 4 shows the comparison of the reproduced experimental results on two benchmark datasets. Finally, Section 5 concludes this work with discussions about the results.

2 Reproducibility approach

In course of specifying the experiment design, we tried to stay as close as possible to the original implementation settings.

First, we needed to get familiar with the key aspects of the hypothesis setting in the original concept paper and the experiment workflow described in the *README* files stored in the author’s GitHub repository. The original code repository has been cloned to our own repository in case for any code adjustment[[1]](#footnote-2).

2.1 Technical framework

Before starting to reproduce results, an Elasticsearch engine needs to be setup. Elasticsearch is a widely used search and analytics engine, which comes especially powerful with huge amounts of data. It can be downloaded from the official elasticsearch website[[2]](#footnote-3), fortunately the version 5.4.0, used for the workflow, is still available. In addition, a few packages should be installed that are stated in the requirements for running the baseline and SetRank scripts:

* Elasticsearch 5.4.0
* Python 3.7
  + Elasticsearch 5.4.0
  + Textblob 0.13.0

After downloading elasticsearch, the following lines need to be inserted into the underlying yaml-file in ***config/elastisearch.yml***, in order to function properly:

* script.inline: true
* script.indexed: true

To start the engine, the batch-file ***bin*/*elasticsearch.bat*** needs to be executed afterwards in a terminal window.

Additionally, a tool called “pytrec\_eval” is used for evaluation. Fortunately, the version was cloned into their github repository. By running the included ***setup.py*** file, the functionalities could be installed?

2.2 Input data

2.2.1 Source data

The original research paper evaluated the proposed unsupervised approach using TREC Genomics Tracks (abbreviated TREC-BIO) data and Semantic Scholar’s query log (abbreviated S2-CS) data. This data was not included in this repository. However, the latest weblinks were provided in the README, such that the TREC-BIO data could be downloaded from a google drive folder[[3]](#footnote-4), whereas the S2-C2 was found on a website[[4]](#footnote-5) .

2.2.1 Query data

The calculations will be done based on the input queries for both data sets, */data/S2-C2/s2\_query.json* for the S2-C2 data and */data/TREC-BIO/trec\_query.json.* In the paper it was mentioned, that 40 out of all 100 queries are entity-set queries for S2-C2. Therefore, this json file needed to be manually split into a file for word queries and one for entity-set queries. This could be achieved by looking at the “ana” key in each line. Ff there was more than one linked entity reference in there, we consider it as entity-set.

1. {"qid": "21", "ana": {"/m/03j0x": 1}, "query": "human computer interaction"}
2. {"qid": "22", "ana": {"/m/064dh3": 1, "/m/031f5p": 1}, "query": "eye movement clustering"}

These are two of the queries from the json file as an example. Number 1 would be considered as word representation, whereas number 2 would be considered as entity representation.

The same strategy is applied to the TREC-BIO data. There 86 out of 100 queries can be observed as entity-set queries.

2.3 Code

In the mentioned GitHub repository, python scripts for all baseline models and the SetRank algorithm can be found. In addition, the calculations for S2-C2 and TREC-BIO are located in separate folders.

2.3.1 Prerequisites

Some adaptions need to be done beforehand in the code. There have been inconsistencies in the given paths. The file actually called TREC-BIO in the data and baseline folder was incorrectly referenced as TREC\_BIO.

Moreover, to be able to run *setrank\_TREC.py*,

* import nltk
* nltk.download('punkt')

needs to be imported additionally in this file.

2.3.2 Index

Before running the algorithm, the appropriate indexes need to be created on the engine. For that purpose, the ***create\_index.py*** should be executed for all four baseline models, BM25, LM-DIR,LM-JM,IB separately, as well as for the SetRank algorithm itself, and everything for both datasets. The index creation files for the baselines are stored in *code/baselines/S2-C2,* and *code/baselines/TREC-BIO.* The index will be created for a specified model by adding the argument -sim to the execution, like: ***python create\_index.py -sim “bm25”*** .  
For SetRank calculations, the index creation file stored in *code/SetRank* and can be called without any arguments: ***python create\_index.py.***

These indexes are just like a skeleton and need to be filled with the data in a next step. For that purpose, the ***index\_data.py*** should be run. Again, for all algorithms and datasets respectively. The scripts are located in the exact same folders specifies previously. For the BM25 baseline the command would be: ***python index\_data.py -sim “bm25”*** . For the SetRank indexes, again no sim-argument has to specified.

Just after this phase, the actual calculations on the data can be done.

2.3.3 Main calculations

The results for the baseline models using the search engine are produced by ***code/baselines/S2-C2/search\_data.py*** and ***code/baselines/TREC-BIO/search\_data.py.*** These scripts take two additional arguments, the model specification again and the mode of querying, which is either “word” for bag-of-words models, “entity” for bag-of-entities, or “both”, the combination the two approaches.  
For BM25 for example, the following command should be executed:

* python search\_data.py -sim “BM25” -mode “word”
* python search\_data.py -sim “BM25” -mode “entity”
* python search\_data.py -sim “BM25” -mode “both”

These steps need to be performed for all 4 different baselines and both datasets.

The SetRank code is located in different files again. For S2-C2, ***code/SetRank/setRank\_ESR.py*** should be considered, and for TREC data ***code/SetRank/setRank\_TREC.py .*** There would be an option for specifying arguments again, the input, output file and parameters, but by default they are already provided. The restructured queries are the input for the calculations, and the results are saved as .run files at the specified location.

2.3.3.1 Parameter Tuning

Separate files for parameter tuning for the SetRank algorithm are given. However, the settings used for the tuning and

2.3.4 Generating and evaluating output results

(…details…)

After evaluation, adequate statistical tests have been conducted.

(…details…)

3 Difficulties

The first unexpected exercise has been to find out that an elasticsearch engine was the basis of this whole process, which has not been clear to us based on the paper and available resources. In addition, as no one of us had experiences with the engine, we first needed to read up on it and go through a cumbersome installation defined by many trials and errors, since it did not simply work after installation. As described in section 2.1, adaptions in the configuration of the elasticsearch were necessary.

Once elasticsearch was setup, some inconsistencies in the code have been detected, like wrong file paths as described in section 2.3.1.

After collecting all the python-based code files, getting the overall structure was challenging as well, since the few independent README’s did not give a clear overview of what is what exactly, how files should be executed and in which order.

Since the original data has not been included in the author’s repository, we expected that it will not be necessary for getting the key results. Nevertheless, it is needed to create the indexes properly in the elasticsearch engine, thus it had to be downloaded in addition by us.

Furthermore, it was obvious how to get to the separate word and entity models for the baseline algorithms. However, the process for SetRank was not conclusive. After investigation and logical connections, we came to the assumption that the queries for the SetRank algorithm where together in one file and needed to be split manually into separate files in order to execute separate word and entity models.

For parameter tuning,

Pytrec\_eval

We were ambitious to execute more profound validation of the concept, i.e. parameter tuning, testing different significant level, or constructing queries on our own. However, based on the limited timeframe and the show-stopper technical obstacles at the beginning of our reproducibility journey, we needed to **moderate our initial goal**. Alternatively, we focused on **investigating the reproducibility of the outcome of the published scientific paper** (i.e. to confirm the numbers and findings reported in the paper).

The authors have spent some effort to document the key steps of the experiment design, however minor but still important steps have been kept on significantly different granularity level. It might come from some generic assumptions from the author perspective, which resulted in a non-comprehensive list of instructions. Basically, our initial conclusion is that the quality of the **experiment process-flow was not adequately documented,** neither in the research paper nor in the git-hub repository. This fact required us to spent significant amount of time until we figured out the missing points.

We also considered reaching out to the authors of the original concept paper, but based on the git-hub issue status, they do not seem to be reachable anymore concerning this project. So, we needed to accept limited possibility for additional or external consultancy.

4 Results and Key findings

Here, we would like to show the outcome of the comparison of the original and the reproduced output results. Additionally, we intend to materialize whether the differences are significant (questioning the original conclusions of the hypothesis) based on statistical significance testing performed using the pytrec\_eval tool.

4.1 Output data recalculation

**Additional details:** Report the numbers obtained in each intermediate step. Identify deviations from the numbers reported in the original paper, their origin, and estimate whether they will have a significant impact on subsequent steps.

For the results, perform adequate tests to test for statistical significance. Justify your choice. Can you confirm the findings of the paper? Did you identify a flaw in their setup? Could you correct the flaw? How did it impact the results and findings of the experiments?

- level of reproducibility,

- while changing these things, what information is gained by successfully reproducing (or failing to reproduce) a study?

xxx

**Table 1: Comparison of the reported and recalculated results of SetRank**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | | BM25 | LM-DIR | LM -JM | IB | SetRank |
| Dataset | Method |  |  |  |  |  |
| S2-C2 | NDCG@5 |  |  |  |  |  |
| NDCG@10 |  |  |  |  |  |
| NDCG@15 |  |  |  |  |  |
| NDCG@20 |  |  |  |  |  |
| TREC-BIO | NDCG@5 |  |  |  |  |  |
| NDCG@10 |  |  |  |  |  |
| NDCG@15 |  |  |  |  |  |
| NDCG@20 |  |  |  |  |  |

xxx

**Table 2: …**

xxx

**Table 3: …**

4.2 Statistical testing

xxx

**Table 4: …**

xxx

**Table 5: …**

5 Conclusions

After reviewing, putting effort into the reproduction and evaluating the final results of the referred original research paper, we came to the following conclusions.

The concept was adequately documented, however the associated source code was not executable straight away. Some adaptions were necessary.

To finally get the results being subject to comparison, some adjustments were necessary to be done which were difficult to be figured out.

Based on the final results, we can conclude that the results …

(…)

Additional details…:

* the information given in the paper is sufficient to reproduce the results reported
* statistically significant differences can be made out between the different settings, in particular when this is not reported in the paper (no significance tests, confidence intervals, p values, etc. or not even variance)
* the values reported in the paper could stem from the distribution sampled by the reproduced experiments

Alternatively:

Our conclusion is that the original **experiment process-flow was not adequately documented** neither in the research paper nor in the linked git-hub repository.

to confirm the numbers and findings reported in the paper or …

Based on the constant bottleneck issues in the technical setup we had not chance to reproduce any results that we could have been used for any result evaluation. Accordingly we cannot make conclusion on the original hypothesis – concerning: whether SetRank algorithm is overperforming traditional search algorithms in case of scientific literatures based on …

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1. <https://github.com/gabortoaso/G10-Research-paper-validation> [↑](#footnote-ref-2)
2. [Download Elasticsearch | Elastic](https://www.elastic.co/de/downloads/elasticsearch) [↑](#footnote-ref-3)
3. [SetRank-dataset – Google Drive](https://drive.google.com/drive/folders/15RqULDGONFfieaOyv40ApKMNEL4vS4V-) [↑](#footnote-ref-4)
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