

SUMPUBMED: Summarization Dataset of PubMed Scientific Articles

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Abstract

Most earlier work on text summarization is carried out on news article datasets. The summary in these datasets is naturally located at the beginning of the text. Hence, a model can spuriously utilize this correlation for summary generation instead of truly learning to summarize. To address this issue, we constructed a new dataset, SUMPUBMED, using scientific articles from the PubMed archive. We conducted a human analysis of summary coverage, redundancy, readability, coherence, and informativeness on SUMPUBMED. SUMPUBMED is challenging because (a) the summary is distributed throughout the text (not-localized on top), and (b) it contains rare domain-specific scientific terms. We observe that seq2seq models that adequately summarize news articles struggle to summarize SUMPUBMED. Thus, SUMPUBMED opens new avenues for the future improvement of models as well as the development of new evaluation metrics.

1 Introduction

Most of the existing summarization datasets, i.e., CNN Daily Mail and DUC are news article datasets. That is, the article acts as a document, and the summary is a short (10-15 lines) manually written highlight (i.e., headlines). In many cases, these highlights have significant lexical overlap with the few lines at the top of the article. Thus, any model which can extract the top few lines, e.g., extractive methods, performs adequately on these datasets.

However, the task of summarization is not merely limited to short-length news articles. One could also summarize long and complex documents such as essays, research papers, and books. In such cases, an extractive approach will most likely fail. For successful summarization on these documents, one needs to (a) find information from the distributed (non-localized) locale in the large

text, (b) perform paraphrasing, simplifying, and shortening of longer sentences and (c) combine information from multiple sentences to generate the summary. Hence, an abstractive approach will perform better on such large documents.

One obvious source that contains such complex documents is the MEDLINE biomedical scientific articles, which are publicly available. Furthermore, these articles are accompanied by abstracts and conclusions which summarize the documents. Therefore, we constructed a scientific summarization dataset from pre-processed PubMed articles, named SUMPUBMED. In comparison to the previous news-article based datasets, SUMPUBMED documents are longer, and the corresponding summaries cannot be extracted by selecting a few sentences from fixed locations in the document.

The dataset, along with associated scripts, are available at <https://github.com/vgupta123/sumpubmed>. Our contributions in this paper are:

- We created a new scientific summarization dataset, SUMPUBMED, which has longer text documents and summaries with non-localized information from documents.
- We analyzed the quality of summaries in SUMPUBMED on the basis of four parameters: readability, coherence, non-repetition, and informativeness using human evaluation.
- We evaluated several extractive, abstractive (seq2seq), and hybrid summarization models on SUMPUBMED. The results show that SUMPUBMED is more challenging compared to the earlier news-based datasets.
- Lastly, we showed that the standard summarization evaluation metric, ROUGE (Lin, 2004), correlates poorly with human evaluations on SUMPUBMED. This indicates the

need for a new evaluation metric for the scientific summarization task.

In Section 1, we provided a brief introduction. The remaining parts of the paper are organized as follows: in Section 2 we explain how SUMPUBMED was created. In Section 3, we explain how summaries were annotated by human experts. We then move on to experiments in Section 4. We next discuss the results and analysis in Section 5, followed by the related work in Section 6. Lastly, we move on to the conclusions in final Section 7.

2 SUMPUBMED Creation

SUMPUBMED is created from PubMed biomedical research papers, which has 26 million documents. The documents are sourced from diverse literature, including MEDLINE, life science journals, and online books. For SUMPUBMED creation we took 33,772 documents from Bio Med Central (BMC). BMC incorporates research papers related to medicine, pharmacy, nursing, dentistry, health care, health services, etc.

The research documents in BMC contain two subsections: *Front* and *Body*. The front part of the document is basically the abstract and taken as the gold summary. The body part which is taken as the main document contains three subsections: background, results, and conclusion.

Preprocessing The average word count in the PubMed scientific articles is around 4,000 words for each document and 250 to 300 lines in every document. Therefore, to create SUMPUBMED, we performed extensive preprocessing so that non-textual content is removed and the overall text is reduced to a more manageable size. This extensive pre-processing step is one of the main factors that sets SUMPUBMED apart from similar datasets (Cohan et al., 2018).

During preprocessing, the non-textual content from the text was removed by: (a) replacing citations and digits in the content with `<cit>` and `<dig>` labels, (b) removing figures, tables, signatures, subscripts, superscripts, and their associated text (e.g., captions), and (c) removing the acknowledgments and references from the text. All the preprocessing was done on a sentence level utilizing the Python regex library.¹ After preprocessing,

¹<https://tinyurl.com/q5v9p5d>

we convert the final document to an XML format and use the SAX parser to parse it.

SAX vs DOM parser: In SAX, events are triggered when the XML is being parsed. When the parser is parsing the XML and encounters a tag starting (e.g., `< something >`), then it triggers the `tagStarted` event (actual name of the event might differ). Similarly, when the end of the tag is met while parsing (`< /something >`), it triggers `tagEnded`. Using a SAX parser implies one needs to handle these events and make sense of the data returned with each event. One could also use the DOM parser,² where no events are triggered while parsing. In DOM the entire XML is parsed, and a DOM tree (of the nodes in the XML) is generated and returned. In general, DOM is easier to use but has a huge *overhead* of parsing the entire XML before one can start using it; therefore, we use SAX instead.

An example of the front part, body part, and the XML file formed from the pre-processed text is shown in <https://github.com/vgupta123/sumpubmed/blob/master/template.pdf>.

Versions of SUMPUBMED We maintained three versions of SUMPUBMED with varying degrees of preprocessing, a) XML, b) Raw Text, and c) Noun-phrases. Details of each version are as follows:

- In the XML version, we exported the whole dataset into a single XML file
- The Raw Text version is obtained after preprocessing when removing non-textual context is completed, followed by XML parsing.
- In the Noun phrases version, we processed the raw text version further to ensure that the summary and the text have the same named entities.

We found that standard Name Entity Recognition (NER) (Finkel et al., 2005) and Biomedical Named Entity Recognizer (ABNER) (Settles, 2005) fail to pick the scientific named entities correctly. Note that the main reason behind ABNER insufficiency is the presence of novel PubMed named entities that were not covered by any of the classes in the ABNER tool. Therefore, we use a simple heuristic of noun intersection between summary and main-text noun phrases to obtain plausible entity sets. This produced a shorter version of both the text and the summary than the original pair.

²<https://tinyurl.com/py6qxzc>

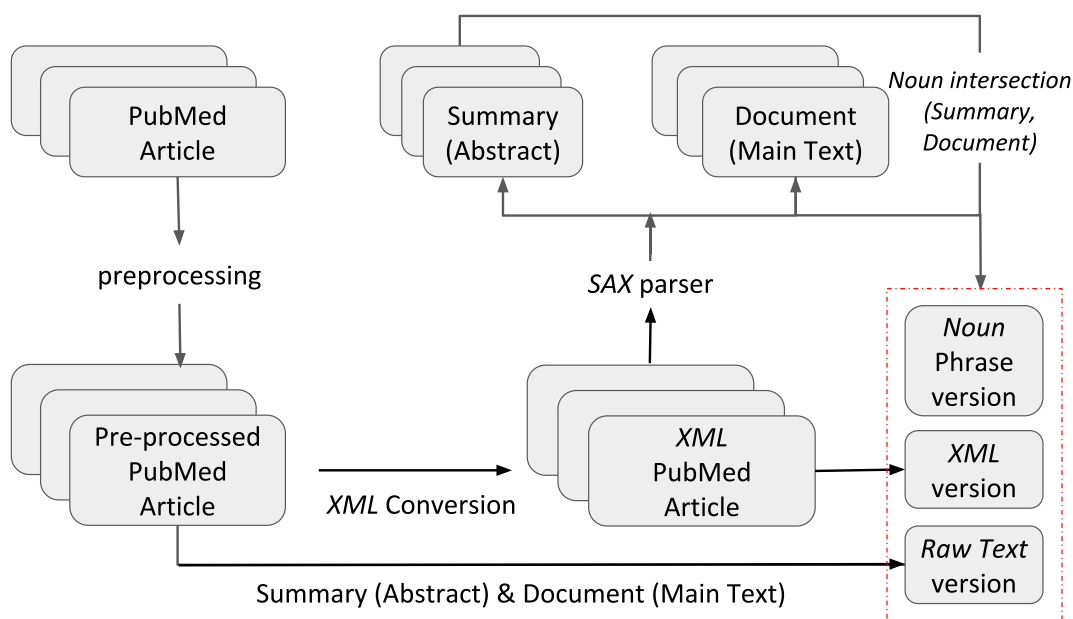


Figure 1: SUMPUBMED creation pipeline.

| Version | Avg. Stats | Summary | Article |
|---------------------|------------|---------|---------|
| Raw Text version | Words | 277 | 4227 |
| | Sents | 14 | 203 |
| Noun Phrase version | Words | 223 | 1578 |
| | Sents | 10 | 57 |
| Hybrid version | Words | 223 | 1891 |
| | Sents | 10 | 71 |

Table 1: Average number of sentences and words in the abstract and text in the three SUMPUBMED versions

The SUMPUBMED versions statistics is given in Table 1. The SUMPUBMED overall creation pipeline is shown in Figure 1.

3 Human Annotation of SUMPUBMED

Inspired from work on human evaluation of summaries by Friedrich et al. (2014), we distributed 50 randomly chosen summaries from the noun-phrase versions of SUMPUBMED to 10 expert annotators (graduate NLP students) such that we have 3 annotation for each summary. We asked these human-annotators to rate the summaries on a scale of 1 to 10. We created different document files, each having 10 pairs of summaries where we randomly shuffled between reference and generated summaries with respect to the placement on the page (left or right). The annotators evaluated the summaries based on the following criteria:

- *Non-Repetition and no factual Redundancy*

(*Non-Re*): There should not be redundancy in the factual information, and no repetition of sentences is allowed.

- *Coherence (Coh)*: Coherence means “continuity of sense”. The arguments have to be connected sensibly so that the reader can see consecutive sentences as being about one (or a related) concept.
- *Readability (Read)*: Consideration of general readability criteria such as good spelling, correct grammar, understandability, etc. in the summaries.
- *Informativeness, Overlap and Focus (IOF)*: How much information is covered by the summary. The goal is to find the common pieces of information via matching the same keywords (or key phrases), such as “Nematodes”, across the summary. For overlaps, annotators compare the keywords’ (or key-phrases) occurrence frequency and ensure the summaries are on the same topic.

The average scores and standard deviations are shown in Table 2. Annotators found that for readability, coherence, and non-repetitiveness, the quality of summaries is satisfactory. However, for informativeness and overlap, it is hard to evaluate summaries due to domain-specific technical terms.

| Criteria | Mean (μ) | S.D. (σ) |
|----------|----------------|-------------------|
| Non-Re | 7.19 | 0.755 |
| Coh | 6.87 | 0.705 |
| Read | 6.82 | 0.821 |
| IOF | 6.31 | 0.879 |

Table 2: Mean and Standard Deviation (SD) scores of human annotation on 50 summaries

ROUGE and Human Scores For the 50 summaries evaluated by expert annotators, we calculated the Pearson’s correlation (Pearson, 1895) between ROUGE (Lin, 2004) scores (ROUGE-1 (R-1), ROUGE-2 (R-2) and ROUGE-L (R-L)) in terms of precision, recall and F1 score with the human-evaluated scores. ROUGE- n is an n -gram similarity measure that computes uni/bi/trigram and higher n -gram overlaps. In R-L, L refers to the Longest Common Subsequence (LCS) overlap: a subsequence of matching words with the maximal length that is common in both texts with the order of words being preserved. Pearson’s correlation value (between -1 and $+1$) quantifies the degree to which quantitative and continuous variables are related to each other. The Pearson’s correlations values are shown in Table 3.

ROUGE scores assume that a high-quality summary generated by a model should have common words and phrases with a gold-standard summary. However, this is not always true because (a) there can be semantically similar meaning (synonymous) word usage, and (b) there can be the usage of text paraphrases (similar information conveyed) with a little lexical overlap in the reference summary text. Therefore, merely considering lexical overlaps to evaluate summary quality is not sufficient. A high ROUGE score may indicate a good summary, but a low ROUGE score does not necessarily indicate a bad summary. Furthermore, while summarizing large documents, humans tend to utilize different paraphrasing/words to convey the same meaning in a shorter form. Several studies by Cohan and Goharian (2016); Dohare et al. (2017) argue that ROUGE is not an accurate estimator of the quality of a summary for scientific input, e.g., biomedical text. Hence, a weak correlation of ROUGE scores with human ratings on SUMPUBMED, as reported in Table 3, should not be a surprise. That is, all correlation values in Table 3 are close to zero, so we can conclude that Rouge scores are weakly related with human ratings on the SUMPUBMED.

4 Experiments

We have used the noun phrase version of SUMPUBMED in the abstractive summarization settings and the Hybrid version of SUMPUBMED in the extractive and the hybrid settings, i.e., (extractive + abstractive) summarizations. We split the dataset into train (93%), test (3%), and validation (4%) sets. Before training, we wrote a script that first tokenizes all input files and then forms the vocabulary and chunked files for the train, test, and validation sets. This step converts the input into a suitable format for the *seq2seq* models.

4.1 Baseline Models

We use the following models on SUMPUBMED for evaluation: We use extractive, abstractive, and hybrid (extractive + abstractive) automatic summarization methods to evaluate SUMPUBMED.

Abstractive Methods We use several modifications of *seq2seq* with attention, as described below:

Seq2Seq with Attention (Nallapati et al., 2016): The encoder is a single layer bidirectional LSTM, while the decoder is a single layer unidirectional LSTM. Both the encoder and decoder have same sized hidden states, with an attention mechanism over the source hidden states and a soft-max layer over the vocabulary to generate the words. We use the same vocabulary for both the encoding and the decoding phase.

Seq2Seq with Pointer Generation Networks (See et al., 2017): The previous model has a computational decoder complexity because each time we have to apply the softmax over the entire vocabulary. The model also outputs an excessive number of UNK tokens (UNK is a special token utilized for out-of-vocabulary words) in the target summary. To address this issue, we use a pointer-generator network (See et al. (2017)) which integrates the basic *seq2seq* model (with attention) with a copying mechanism (Gu et al. (2016)). We call this model *seq2seq* for the rest of the paper.

The seq2Seq model with Pointer Generation Networks and Coverage Mechanism (+cov) (Mi et al., 2016): The summaries generated by the model discussed before may show repetition, like generating the same arrangement of words multiple times (e.g., “this bioinformatic approach this bioinformatic approach...”). This repetition of phrases is prominent when generating multi-line summaries. The solu-

| Criteria | Prec | | | Recall | | | F1 | | |
|----------|-------|-------|-------|--------|-------|--------|--------|--------|-------|
| | R-1 | R-2 | R-L | R-1 | R-2 | R-L | R-1 | R-2 | R-L |
| Non-Re | -0.09 | -0.06 | -0.11 | +0.02 | -0.07 | +0.007 | +0.008 | -0.05 | +0.03 |
| Coh | +0.05 | -0.14 | +0.05 | -0.04 | -0.25 | -0.01 | +0.02 | -0.19 | +0.06 |
| Read | +0.19 | +0.09 | +0.20 | +0.006 | -0.03 | +0.03 | +0.12 | +0.01 | +0.13 |
| IOF | -0.15 | -0.18 | -0.16 | +0.12 | 0.08 | +0.09 | +0.06 | -0.007 | +0.12 |

Table 3: Pearson’s correlation between ROUGE scores and human ratings on SUMPUBMED’s noun-phrase version

tion to the problem of redundancy in summaries in seq2seq models is the coverage mechanism of Mi et al. (2016). This model penalizes repeated word generations by keeping track of the hitherto covered parts using attention distribution.

Extractive Methods There are several existing approaches to extractive summarization, mostly derived from LexRank (Erkan and Radev, 2004), and TextRank (Mihalcea and Tarau, 2004). We use TextRank, which is an unsupervised approach for sentence extraction, and has been used successfully in many NLP applications (Hulth, 2003).

Hybrid Methods (Extractive + Abstractive) We also experimented with the hybrid approach for summarization. First, we used extractive summarization using the TextRank ranking algorithm. We then applied abstractive summarization on the extracted text. We used the pointer-generator networks, followed by the coverage mechanism for the abstractive summarization. In this setting, we have not performed any preprocessing before extractive summarization to decrease the length of the documents. The extractive summarization step makes the text length sufficient to apply the abstractive summarization step on it quite easily.

4.2 Experimental Settings

While decoding seq2seq models (for abstractive and hybrid models), we use a beam search (Medress et al., 1977) with a beam width of 4. Note that, Beam search is a greedy technique which chooses the most likely token from all generated tokens at each step to obtain the best b sequences (the hyper-parameter b here represents the beam width). Beam search is shown to be better than generating the first sequence.

We also experimented with varying target summary lengths (i.e., the number of decoding steps) for seq2seq models. We report both seq2seq models with and without coverage results for comparison. We considered ROUGE-1 (R-1), ROUGE-2 (R-2), and ROUGE-L (R-L)’s precision, recall, and

F1 score for evaluation.

Hyper-parameters The hyper-parameters used for the seq2seq model is in Table 4.

| Hyper-parameter | Value |
|---------------------------|----------|
| LSTM Hidden state size | 256 |
| Word embedding dimensions | 128 |
| Batch Size | 16 |
| encoder steps training | 100-1000 |
| encoder steps testing | 100-4000 |
| decoder steps length | 100-250 |
| beam size | 4 |
| learning rate for adagrad | 0.15 |
| maximum gradient norm | 2.0 |

Table 4: Hyper-parameters for seq2seq models

We utilized tensorflow package³ for models and ROUGE evaluation package pyrouge⁴ for the evaluation metric. We use a single *GeForce GTX TITAN X* with 12GB GPU memory taking on average 5 to 6 days per model for model training.

5 Results and Analysis

Results on SUMPUBMED for abstractive methods, i.e., seq2seq models (with and without coverage), the extractive method of TextRank, and the hybrid approach, i.e., TextRank + seq2seq (with and without coverage) are shown in Tables 6, 7, and 8, respectively. We also evaluated the seq2seq models on news datasets (CNN/Daily Mail and DUC 2001) for comparison, as shown in Table 5.

Analysis: In all three approaches, abstractive in Table 6, extractive in Table 7 and hybrid in Table 8, we notice that the ROUGE Recall and F1-score increase, whereas precision decreases with the number of words (100 to 250) in the target summaries. The increase in Recall is expected as the chances of lexical overlap are more with larger generated summaries. Precision decreases because, with more

³<https://www.tensorflow.org/>

⁴<https://pypi.org/project/pyrouge/>

| Data | Model | R-1 | | | R-2 | | | R-L | | |
|--------|---------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| | | Pr | Re | F1 | Pr | Re | F1 | Pr | Re | F1 |
| CNN-DM | seq2seq | 33.49 | 38.49 | 34.61 | 13.89 | 15.87 | 14.29 | 30.15 | 34.64 | 31.15 |
| | +cov | 38.59 | 41.10 | 38.53 | 16.84 | 17.83 | 16.75 | 35.56 | 37.81 | 35.48 |
| DUC | seq2seq | 41.34 | 21.33 | 27.63 | 14.28 | 7.30 | 9.49 | 32.95 | 16.93 | 21.93 |
| | +cov | 43.86 | 21.92 | 28.57 | 15.04 | 7.41 | 9.68 | 34.96 | 17.29 | 22.60 |

Table 5: ROUGE scores on CNN-Dailymail (CNN-DM) and DUC 2001 dataset (DUC) using seq2seq models

| Steps | Model | R-1 | | | R-2 | | | R-L | | |
|-------|---------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| | | Pr | Re | F1 | Pr | Re | F1 | Pr | Re | F1 |
| 100 | seq2seq | 52.30 | 20.56 | 28.01 | 16.01 | 6.17 | 8.50 | 47.97 | 18.70 | 25.53 |
| | +cov | 57.50 | 22.66 | 31.04 | 20.28 | 7.74 | 10.73 | 52.62 | 20.56 | 28.23 |
| 150 | seq2seq | 48.88 | 27.10 | 32.81 | 15.18 | 8.35 | 10.18 | 44.64 | 24.56 | 29.81 |
| | +cov | 55.11 | 29.71 | 36.79 | 19.17 | 10.14 | 12.66 | 50.48 | 27.07 | 33.57 |
| 200 | seq2seq | 44.83 | 30.23 | 33.79 | 13.73 | 9.20 | 10.33 | 40.86 | 27.37 | 30.65 |
| | +cov | 52.86 | 33.84 | 39.21 | 18.25 | 11.52 | 13.43 | 48.47 | 30.88 | 35.84 |
| 250 | seq2seq | 41.18 | 31.84 | 33.00 | 12.80 | 9.79 | 10.22 | 37.68 | 28.89 | 30.03 |
| | +cov | 51.11 | 36.24 | 40.13 | 17.63 | 12.39 | 13.77 | 46.92 | 33.13 | 36.73 |

Table 6: ROUGE scores of noun-phrase SUMPUBMED version using a seq2seq model of varying decoding steps

| Steps | R-1 | | | R-2 | | | R-L | | |
|-------|--------------|--------------|--------------|--------------|--------------|--------------|-------|-------|--------------|
| | Pr | Re | F1 | Pr | Re | F1 | Pr | Re | F1 |
| 150 | 45.91 | 31.69 | 36.82 | 16.97 | 11.09 | 13.12 | 39.12 | 26.91 | 28.84 |
| 200 | 42.81 | 36.03 | 38.44 | 15.71 | 13.31 | 14.10 | 36.60 | 30.73 | 31.48 |
| 250 | 40.51 | 39.59 | 39.33 | 14.81 | 15.30 | 14.72 | 34.83 | 33.98 | 34.83 |

Table 7: Results for TextRank an Extractive Summarization approach on hybrid version of the SUMPUBMED.

| Steps | Model | R-1 | | | R-2 | | | R-L | | |
|-------|---------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| | | Pr | Re | F1 | Pr | Re | F1 | Pr | Re | F1 |
| 100 | seq2seq | 50.32 | 21.09 | 28.45 | 12.66 | 5.14 | 7.04 | 46.58 | 19.40 | 26.23 |
| | +cov | 56.07 | 27.42 | 30.69 | 16.65 | 6.47 | 8.95 | 51.87 | 20.62 | 28.27 |
| 150 | seq2seq | 45.01 | 25.50 | 30.99 | 11.14 | 6.21 | 7.59 | 41.43 | 23.35 | 28.42 |
| | +cov | 52.23 | 29.11 | 35.62 | 15.44 | 8.45 | 10.42 | 48.35 | 26.81 | 32.86 |
| 200 | seq2seq | 40.55 | 28.46 | 31.56 | 9.93 | 6.93 | 7.70 | 37.21 | 25.98 | 28.86 |
| | +cov | 47.82 | 33.37 | 37.28 | 14.01 | 9.68 | 10.84 | 44.29 | 30.80 | 34.44 |
| 250 | seq2seq | 35.80 | 30.88 | 30.61 | 9.14 | 7.67 | 7.66 | 32.67 | 27.95 | 27.80 |
| | +cov | 43.82 | 36.16 | 37.33 | 12.77 | 10.49 | 10.85 | 40.55 | 33.37 | 34.49 |

Table 8: ROUGE scores on hybrid version of the SUMPUBMED using Hybrid model: TextRank + seq2seq models

| Model | R-1 | | | R-2 | | | R-L | | |
|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|
| | Pr | Re | F1 | Pr | Re | F1 | Pr | Re | F1 |
| Abstractive | 51.11 | 36.24 | 40.13 | 17.63 | 12.39 | 13.77 | 46.92 | 33.13 | 36.73 |
| Extractive | 40.51 | 39.59 | 39.33 | 14.81 | 15.30 | 14.72 | 34.83 | 33.98 | 32.82 |
| Hybrid Model | 43.82 | 36.16 | 37.33 | 12.77 | 10.49 | 10.85 | 40.55 | 33.37 | 34.49 |

Table 9: ROUGE comparison on SUMPUBMED. seq2seq abstractive methods' target summary is of 250 words

words, the chances of non-covered words in the output summary also increase.

the coverage (+cov) mechanism, the problem of repetition in summaries is solved to a great extent. The ROUGE scores also show improvement after

We notice in both Tables 6 and 8 that by adding

applying coverage to pointer-generator networks. Thus, one can conclude that pointer generator networks effectively handle named entities and out-of-vocabulary words, and the coverage mechanism is useful to avoid repetitive generation, which is essential for scientific summarization.

In Table 9, we note that in terms of Precision (Pr), the abstractive approach shows the best results. However, the Recall (Re) of the extractive summarization model is always better than abstractive and hybrid approaches. Furthermore, the R-1 Re (ROUGE-1 Recall) and R-L Re (ROUGE-L Recall) for the hybrid models are approximately similar to the abstractive models. We also provide a few qualitative example of summarization on CNN/DailyMail in Appendix Section A, on SUMPUBMED in Appendix Section B.

6 Related Work

Below, we provide the details of other summarization datasets:

News: CNN-Daily Mail has 92,000 examples with documents of 30-sentence length with 4 corresponding human-written summaries of 50 words. DUC (Document Understanding Conference), another dataset, contains 500 documents (35.6 tokens on average) and summaries (10.4 tokens). Gigaword (Rush et al., 2015) has 31.4 document tokens and 8.3 summary tokens. Lastly, X-Sum (Extreme Summarization) (Narayan et al., 2018) contains 20-sentence (BBC articles) (431 words) and corresponding one-sentence (23 words) summaries.

Social Media: Webis-TLDR-17 Corpus (Völske et al., 2017) is a large-scale dataset of 3 million pairs of content and self-written summaries obtained from social media (Reddit). Webis-Snippet-20 Corpus (Chen et al., 2020) contains 10 million (webpage content and abstractive snippet) pairs and 3.5 million triples (query terms, abstractive snippets, etc.) for query-based abstractive snippet generation of web pages.

Scientific: Recently, Sharma et al. (2019) released a large dataset of 1.3 million of U.S. patent documents along with human written summaries. However, the closest datasets to SUMPUBMED are released by Cohan et al. (2018); Kedzie et al. (2018); Gidiotis and Tsoumakas (2019).

Comparison with SUMPUBMED: News datasets' summary is located at the top of

the article for most examples. Social media datasets lack the scientific aspect, i.e., complex domain-specific vocabulary and non-localized distributed information of SUMPUBMED. Other works on the scientific datasets are by Cohan et al. (2018); Kedzie et al. (2018); Gidiotis and Tsoumakas (2019). The closest work to our approach is the PubMed dataset by Cohan et al. (2018). However, unlike SUMPUBMED, (a) no extensive preprocessing pipeline was applied to clean the text (b) a single version is released compared with SUMPUBMED's several versions with distinct properties (varying summary lengths, article lengths, and vocabulary sizes), (c) only level-1 section headings instead of the whole PubMed document are used, and (d) there is a lack of human evaluation to assess data quality. However, Cohan et al. (2018) do act as an powerful inspiration for our work.

7 Conclusion

We created a non-news, SUMPUBMED dataset, from the PubMed archive to study how various summarization techniques perform on task of scientific summarization on domain specific scientific texts. These texts have essential information scattered throughout the whole text. In contrast, earlier datasets with news stories appear to mostly have useful information in the first few lines of the document text. We also conducted a human evaluation on aspects such as repetition, readability, coherence, and Informativeness for 50 summaries of 250 words. Each summary is evaluated by 3 different individuals on the basis of four parameters: readability, coherence, non-repetition, and informativeness. Due to the unavailability of any state-of-the-art results on this new dataset, we built several baseline models (extractive, abstractive, and hybrid model) for SUMPUBMED. To check the significance of our results, we studied the effectiveness of ROUGE through Pearson's correlation analysis with human-evaluation and observed that many variants of ROUGE scores correlate poorly with human evaluation. Our results indicate that ROUGE is possibly not a proper metric for SUMPUBMED.

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A Summarization Example on CNN/DailyMail Dataset

We see factual redundancy and repetitiveness in the generated summaries with pointer-generation which is removed by applying coverage. In the example below the Factual Redundancy is shown with the bold text:

Reference Summary maricopa county sheriff 's office in arizona says robert bates never trained with them. " he met every requirement , and all he did was give of himself, "his attorney says. tulsa world newspaper: three supervisors who refused to sign forged records on robert bates were reassigned.

Summary from seq2seq some supervisors at the tulsa county sheriff's office were told to forge reserve deputy robert bates ' training records. some supervisors at the tulsa county sheriff's office were told to forge reserve deputy robert bates' training records, and three who refused were reassigned to less desirable duties. **some supervisors at the tulsa county sheriff 's office were told to forge reserve deputy robert bates ' training records.**

Summary from seq2seq with coverage some supervisors at the tulsa county sheriff 's office were told to forge reserve deputy robert bates ' training records . the volunteer deputy 's records had been falsified emerged " almost immediately " from multiple sources after bates killed eric harris on april 2 . bates claims he meant to use his taser but accidentally fired his handgun at harris instead.

B Example of Summarization on SUMPUBMED

Here we provide representative examples of actual summaries. Repetitiveness, i.e., factual redundancy is shown with the bold text.

B.1 Abstractive Summarization on SUMPUBMED

We see factual redundancy and repetitiveness in the generated summaries with pointer-generation which is removed by applying coverage. We also observe that repetitiveness is removed by using the coverage mechanism.

reference: the origin of these genes has been attributed to horizontal gene transfer from bacteria, although there still is a lot of uncertainty about the origin and structure of the ancestral ghf <dig> ppn endoglucanase. our data confirm a close relationship between pratylenchus spp. furthermore, based on gene structure data, we inferred a model for the evolution of the ghf <dig> endoglucanase gene structure in plantparasitic nematodes. our evolutionary model for the gene structure in ppn ghf <dig> endoglucanases implies the occurrence of an early duplication event, and more recent gene duplications at genus or species level. the latter one is the first gene isolated from a ppn of a different superfamily -LRB- sphaerularioidea -RRB-; all previously known nematode endoglucanases belong to the superfamily tylenchoidea -LRB- order rhabditida -RRB-. no statistical incongruence between the phylogenetic trees deduced from the catalytic domain and the cbm <dig> was found, which could suggest that both domains have evolved together. and the root knot nematodes, while some radopholus similis endoglucanases are more similar to cyst nematode genes. two new endoglucanases from the migratory nematodes pratylenchus coffeae and ditylenchus africanus were included in this study. phylogenetic analyses were conducted with the ppn ghf <dig> endoglucanases and homologous endoglucanases from bacterial and other eukaryotic lineages such as beetles, fungi and plants. previous studies on the evolution of these genes have focused primarily on data of sedentary nematodes, while in this study, extra data from migratory nematodes were included. it is not clear whether this ancestral endoglucanase consisted of the whole gene cassette, containing a catalytic domain and a carbohydratebinding module -LRB- cbm, type <dig> in ppn and bacteria -RRB- or only of the catalytic domain while the cbm <dig> was retrieved by domain shuffling later in evolution. the ghf <dig> catalytic domain and the cbm <dig> rather than that it evolved by domain shuffling. endo <dig> betaglucanases or cellulases from the glycosyl hydrolase family <dig> -LRB- ghf5 -RRB- have been found in numerous bacteria and fungi, and recently also in higher eukaryotes, particularly in plantparasitic nematodes -LRB- ppn -RRB-.

seq2seq: although the hox cell line with peculiar properties of horizontal gene transfer -LRB- hgt -RRB- has been proposed to delineate the function of ghf <dig> endoglucanases. the gene structure of the ppn ghf <dig> endoglucanases is a matter of debate, in this study no support for an early exon/domain shuffling event after the independent gain of a catalytic domain. the exon/intron gene structure of the ppn ghf <dig> endoglucanases was compared with the multiple protein sequence alignment. the gene structure of the ppn ghf <dig> endoglucanases was compared with the multiple protein sequence alignment. **the gene structure of the ppn ghf <dig> endoglucanases was compared with the multiple protein sequence alignment. the gene structure of the ppn ghf <dig> endoglucanases was compared with the multiple protein sequence alignment.** the evolution of the gene structure of the ppn ghf <dig> gene families: the number of members from an ancient or early eukaryotic ancestral gene is associated with the expansion of members from an ancient or early eukaryotic ancestral gene. in this study, we.

seq2seq coverage: the expansion of horizontal gene transfer -LRB- hgt -RRB- events in horizontal gene transfer -LRB- hgt -RRB- has been proposed to explain the origin of ghf <dig> endoglucanases in the nematode kingdom. while the ppn ghf <dig> endoglucanases has a close relationship to the root knot nematodes. in order to have a broader overview of the endoglucanase evolution in the infraorder tylenchomorpha, the gene structure of six additional genes was incorporated in our study. the ppn ghf <dig> gene family is associated with the expansion of the ppn ghf <dig> gene family bordered by intron <dig> and intron <dig> although 1 - <dig> symmetrical domains are suggested to be frequently associated with domain shuffling events in the evolution of paralogous gene families: the evolution of the ppn indicate a history of recent duplication events for which little information is available. our model implies that the divergence of the gene structure of the ppn ghf <dig> gene family is notably dynamic, and this evolution involves more intron gains than losses in the order rhabditida -LRB- infraorder tylenchomorpha -RRB-, which is part of one of the three evolutionary independent plantparasitic nematode clades. our results demonstrate that the conserved gene structure of the ppn ghf <dig> endoglucanases and the observation of some sequence conservation in the evolution of the plantparasitic bacteria and nematodes. our results suggest that the evolution of the ghf <dig> gene family is a major consequence of the evolution of.

B.2 Extractive Summarization on SUMPUBMED

TextRank produces a purely extractive summary. But we see that it is able to identify the relevant sentences. The content overlap between the reference and generated extractive summary is adequate.

reference : to find out the different ovarian activity and follicle recruitment with mirnamediated post-transcriptional regulation, the small rnas expressed pattern in the ovarian tissues of multiple and uniparous anhui white goats during follicular phase was analyzed using solexa sequencing data. <dig> mirnas coexpressed, <dig> and <dig> mirnas specifically expressed in the ovaries of multiple and uniparous goats during follicular phase were identified. in the present study, the different expression of mirnas in the ovaries of multiple and uniparous goats during follicular phase were characterized and investigated using deep sequencing technology. rt-pcr was applied to detect the expression level of <dig> randomly selected mirnas in multiple and uniparous hircine ovaries, and the results were consistent with the solexa sequencing data. micrnas play critical roles in almost all ovarian biological processes, including folliculogenesis, follicle development, follicle atresia, luteal development and regression. the result will help to further understand the role of mirnas in kidding rate regulation and also may help to identify mirnas which could be potentially used to increase hircine ovulation rate and kidding rate in the future. the <dig> most highly expressed mirnas in the multiple library were also the highest expressed in the uniparous library, and there were no significantly different between each other. **the highest specific expressed mirna in the multiple library was mir29c, and the one in the uniparous library was mir<dig>** <dig> novel mirnas were predicted in total. superior kidding rate is an important economic trait in production of meat goat, and ovulation rate is the precondition of kidding rate. go annotation and kegg pathway analyses were implemented on target genes of all mirna in two libraries.

extracted : in order to identify differentially expressed mirna during follicular phase in the ovaries of multiple and uniparous anhui white goats, two small rna libraries were constructed by solexa sequencing. for all mirnas target genes of multiple and uniparous goats in the ovaries during follicular phase, there were <dig> and <dig> target genes mapped to the go terms of cellular component. the expression levels of <dig> randomly selected mirnas were verified in the ovaries of multiple and uniparous goats during follicular phase using rt-pcr. in this study, we sequenced the small rnas **in the ovarian tissues of multiple and uniparous anhui white goats during follicular phase** by illumina solexa technology, then analyzed the differentially expressed mirnas, predicted novel mirnas, and made go enrichment and kegg pathway analysis of target genes in two mirna libraries. in ovaries between multiple and uniparous goats of follicular phase, <dig> novel mirnas were predicted in total, which is distinctly more than the amount predicted in our previous study implemented by our team workers, zhang et al. **the highest specific expressed mirna in multiple library was mir29c, and the one in uniparous library was mir<dig>** as aligning the clean reads to the mirna precursor/mature mirnas of all animals in the mirbase <dig> database, and obtained mirna with no specified species. rt-pcr was carried out to analyze the expression of <dig> randomly selected mirnas in multiple and uniparous hircine ovaries during follicular phase, and the results were consistent with the solexa sequencing data.

B.3 Attention Visualization for SUMPUBMED

We can visualize the attention projection for seq2seq models by highlighting the respective words in yellow on the source document while producing a word. Figures 2 and 3 show the words in green with high generation probability, i.e, $p_{gen} > 0.5$ (not copied), non marked words have $p_{gen} < 0.5$ (mostly copied).

Observations While producing a word in the output, we can visualize the respective words in the source document on which the network is focussing. The darker the green highlight over a word in the summary, the higher is the p_{gen} probability. E.g., there is a chance that p_{gen} is high whenever a new sentence is started after a period (.). The model generally focuses on two or three words at a time. There is a high chance that the summary starts with a noun phrase or a noun. For example, we can see in Figure 2 that the summary starts with name (noun) ‘kevin pietersen’.

Article

it 's the picture some england cricket fans have been waiting to see and others have been equally dreading : kevin pietersen back at surrey . the 34-year-old returned to nets on monday for the first time since re-signing for the county last month . he arrived early for the session at the oval - tweeting a picture of the pitch with the caption : ' in the office today . # oval ' - before team-mates such as garth batty and jade dernbach followed him in . kevin pietersen is pictured leaving the oval for the first time since resigning for surrey last month . pietersen returned to nets at surrey on monday and left the oval after training finished just before 2pm . pietersen was pictured driving away from the oval in his expensive telsa sports car . pietersen managed a wry smile as he drove away after training on monday afternoon . pietersen was later pictured leaving the ground just before 2pm and is expected to step-up his county rehabilitation with a three-day warm-up against oxford mccu on april 12 . ultimately , pietersen is hoping to impress enough for surrey to earn a re-call to the england side - possibly for this summer 's ashes rematch - having been sacked by the national side in 2014 . england left for the west indies for their upcoming test series on thursday , with coach peter moores leaving kp in no doubt that he still has a lot to prove - despite incoming england and wales cricket board chairman colin graves appearing to extended an olive branch to the exiled batsman . asked at gatwick about pietersen 's situation , moores said : ' from my point of view , kevin is n't on the radar . '

Reference summary

kevin pietersen took part in a net session at the oval on monday . he is expected to play in three-day game against oxford mccu on april 12 . pietersen has returned to county game to boost chances of england recall .

Generated summary (highlighted = high generation probability)

kevin pietersen returned to nets on monday for the first time since resigning for surrey last month . he returned to nets at surrey on monday and left the oval after training on monday . pietersen is hoping to impress enough for surrey to earn a re-call to the england side .

Figure 2: Attention Probability for decoding on DUC 2001 dataset example, showing the summary is more inclined to an extractive nature. Attention corresponding to the word 'pietersen' present in the generated summary is shown.

Article

in line with these results , pet studies using transient reduction of tinnitus by lidocaine also revealed significantly increased rcbf in temporoparietal cortical activity during tinnitus perception . regarding cortical excitability measures , significantly enhanced intracortical facilitation of the motor cortex , was found in tinnitus patients using transcranial magnetic stimulation . single sessions of rTMS were applied at high frequencies and resulted in a short-lasting but significant improvement , whereas low frequencies have been used for approximately 5 - or 10-day treatment trials and showed a long-lasting reduction in symptoms . comparison of the effect of high - and low-frequency rTMS showed that brief high frequency rTMS has no effect , whereas prolonged low frequency rTMS has a significant effect on tinnitus . , chronic tinnitus sufferers showed surprisingly , that both the high and low-frequency rTMS applications were effective . the largest double-blind parallel study compared the effects of different frequencies of rTMS -RRB- , given daily over the left temporoparietal cortex for weeks . preconditioning the temporal cortex with high-frequency rTMS before low-frequency stimulation did not result in more pronounced effects . recently a specific rTMS paradigm , namely theta-burst stimulation was developed to modulate human primary motor cortex excitability . recently , it has been demonstrated that rTMS applied in bursts of five pulses at 40 Hz repeated at 40 Hz over the auditory cortex has significantly stronger effects on narrow band/white noise tinnitus than tonic Hz stimulation . the aim of the current study was to investigate the effects of all three tbs paradigms in a randomized , single-blinded , cross-over design on tinnitus perception in patients with chronic tinnitus . on the basis of previous reports regarding the use of conventional low - and high-frequency rTMS in tinnitus we hypothesized that single sessions of 40 - sec tbs would also be able to produce a transient attenuation of tinnitus perception . this hypothesis was supported by a recent report that tbs results in comparable after-effects on m excitability when compared with conventional high - and low-frequency rTMS , yet being still more applicable for blinded studies and having a protocol of much shorter duration . the non-parametric friedman anovas , calculated for all the patients for every time point separately , also showed no significant effect of stimulation . wilcoxon matched pairs tests calculated for each tbs protocol separately , resulted in a significant difference only in case of ctbs between baseline and the time point immediately after the stimulation fig in the present study we could not find any significantly different effect on tinnitus perception for the different types of tbs applied to the inferior temporal cortex , either at the lower intensities of 80 % amT , nor at the higher intensities of 80 % rmt . the intensity of the stimulation also did not significantly differ between the two groups that may indicate that the observed slight effects are not intensity dependent , and that the loudness of the noise evoked by the stimulation did not influence the patients . the first possible explanation is that tbs had no effect in our study over the temporal cortex because it could not reach the tinnitus-related areas or was not sufficient to induce excitability changes in these areas . we chose to stimulate all our patients on the left side of the head , over the t eeq-electrode position , irrespective of their tinnitus - affected side , as the primary studies reported positive effects on tinnitus after rTMS over t or very close to it . however , even this enhanced stimulation intensity did not result in better effects on tinnitus perception . stimulation of the temporal cortex with tbs at rmt or above , or using a higher number of impulses was regarded as unsafe by our own safety guidelines , and due to the need for clear safety limits for tbs , safety limits of conventional rTMS should also be applied . if tbs applied over the left inferior temporal cortex was actually not effective on tinnitus , we should consider that all of our non-significant but not negligible observed effects were caused by the placebo effect . it is important to mention that the placebo effect is high in most of the clinical rTMS studies , regardless of the paradigm used . still , with the exception of huang and colleagues , who published the first series of tbs experiments on the motor cortex and stated that mtbs has no effect , there has been no other study , which has confirmed this . in a recent study we found , that mtbs applied over the primary somatosensory cortex has a significant effect on the n component of the laser-evoked potential , but not the sham protocol . therefore , another possible explanation as to why tbs had no significant effect on tinnitus in our study may be that there was no adequate placebo condition ; which is another limitation of our study . the results of the experiments using single trains of tbs suggest that in the human motor cortex tbs produces a mixture of facilitatory and inhibitory effects on synaptic transmission . it is possible that the difference in effectiveness observed between the protocols on motor and sensory cortices could be due to differences in the physiological and functional states of the stimulated cortex . furthermore , several studies have shown that both low - and high-frequency rTMS reduce tinnitus indicating that tms effects on motor cortex excitability are different from tms effects on tinnitus perception . one session of rTMS has only very short-lasting effects on tinnitus perception . furthermore women experience greater suppression of their tinnitus with burst stimulation than men and since we had only two women , it could influence our results . our study design and results do not allow us to draw conclusion about the neuronal mechanisms of tms on the temporal cortex , but may show that the effects of tms on tinnitus are not directly mediated by tms induced modulation of excitability in the stimulated cortical area . it is important to note that in previous studies using high-frequency suprathreshold rTMS , the improvement in tinnitus was observed by about 42 - 68 % of the stimulated patients . according to the recent results of rTMS applied in alpha - , beta - , and theta-bursts , new types of burst stimulation protocols may be more effective in tinnitus .

Reference summary

although half of the patients reported a slight attenuation of tinnitus perception , group analysis resulted in no significant difference when comparing the three specific types of tbs . in addition there was no significant difference when comparing the responder and !!non-responder!! groups regarding their !!anamnesitic!! and !!audiological!! data . repetitive transcranial magnetic stimulation over the temporoparietal cortex was recently introduced to modulate tinnitus perception . changes in subjective tinnitus perception were measured with a numerical rating scale . patients received pulses of continuous tbs , intermittent tbs and intermediate tbs over left inferior temporal cortex with an intensity of 80 % of the individual active or resting motor threshold . in the current study , the effect of theta-burst stimulation , a novel rTMS paradigm was investigated in chronic tinnitus . cortical excitability changes as well as imbalances in excitatory and inhibitory circuits play a distinct pathophysiological role in chronic tinnitus . tbs applied to inferior temporal cortex appeared to be safe . twenty patients with chronic tinnitus completed the study . the tQ score correlated significantly with the vas , lower loudness indicating less tinnitus distress .

Generated summary (highlighted = high generation probability)

The effect of the second month of the indirect brain barrier for the medial edge of the medial edge confirms the importance of medial prefrontal cortex and evoked potentials . the intensity of tms induced modulation of tinnitus - and lidocaine motion were observed in patients with painful subjective development . we investigated the effects of all three tbs paradigms in a randomized , single-blinded cross-over design . the aim of this study was to investigate the neuronal mechanisms of tms on the temporal cortex of tinnitus perception in patients with chronic tinnitus perception . in this study , we investigated the effects of the temporal cortex with high-frequency suprathreshold rTMS on motor cortex excitability and functional states of the stimulated cortical area tbs at Hz over the left inferior temporal cortex . and compared to the inferior frontal cortex , and then subjected to the placebo group . the placebo effect was evaluated using single trains of tbs , using high-frequency suprathreshold rTMS as a mixture of the n component of the stimulated cortical area . the results of the present study suggest that tms effects on tinnitus after low-frequency stimulation than men did not differ in the physiological and functional states of the stimulated cortical area . in the present study , we investigated the effects of rTMS on the left side of the somatosensory cortex and over the left inferior frontal gyrus . we found that the observed effects of rTMS resulted in a significant

Figure 3: Attention Probability for decoding on a SUMPUBMED example where the attention corresponding to word 'present' in the generated summary is shown.