

Mini Project 2 Report
on
**Sequence-to-sequence networks for multi-text document
summarization**

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CERTIFICATE

It is certified that the work contained in the project report titled “Sequence-to-sequence networks for multi-text document summarization” by “Arjun Sagar N V (20BCS020)”, “Harshith R N (20BCS056)” and “B.Jagadish Chandra (20BCS032),” has been carried out under my/our supervision and that this work has not been submitted elsewhere for a degree.

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We declare that this written submission represents my ideas in my own words and where others' ideas or words have been included, we have adequately cited and referenced the original sources. We also declare that we have adhered to all principles of academic honesty and integrity and have not misrepresented or fabricated or falsified any idea/data/fact/source in our submission. We understand that any violation of the above will be cause for disciplinary action by the Institute and can also evoke penal action from the sources which have thus not been properly cited or from whom proper permission has not been taken when needed.

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1 Abstract

In the ever-expanding field of medical research, the volume of available documents and literature is overwhelming. Efficiently summarizing multiple texts into concise and informative summaries is crucial for researchers, healthcare professionals and policymakers. This research explores the application of sequence-to-sequence networks for multi-text document summarization in the medical domain. We introduce a novel approach that makes use of deep learning and natural language processing techniques to extract essential information from a collection of medical documents. Sequence-to-sequence networks are a particular kind of neural network architecture intended for sequential input, and we use them in our research, to generate coherent and accurate summaries. This research contributes to the ongoing efforts in utilizing advanced machine learning techniques to facilitate knowledge extraction and dissemination in the medical domain. The proposed approach holds promise for aiding healthcare professionals, researchers and decision-makers in staying updated with the latest developments and findings, ultimately fostering advancements in medical research and patient care.

2 Introduction

The field of medicine is evolving at an unprecedented pace, generating a vast amount of textual data in the form of research papers, clinical reports and medical publications. Keeping abreast of this ever-expanding knowledge landscape is essential for healthcare professionals, researchers and policymakers. Nonetheless, the amount of medical literature available might be overwhelming, making it challenging to extract meaningful insights efficiently. Multi-text document summarization in the medical domain addresses this challenge by providing concise, coherent and informative summaries of multiple documents, enabling professionals to grasp the essence of extensive research quickly.

In recent years, the advent of advanced NLP (Natural Language Processing) techniques has significantly enhanced the capabilities of automatic text summarization. Traditional methods often struggle to capture the complexity of medical texts, which are replete with specialized terminology, intricate concepts, and diverse writing styles. To tackle these complexities, researchers have explored innovative approaches, employing sophisticated algorithms and ML (machine learning) models to distill essential information from a multitude of medical documents. Effectively summarizing multiple medical documents is crucial for extracting valuable insights, staying updated with the latest research, and making informed decisions. The complexity of medical texts is often too much for traditional text summarization techniques to handle, such as specialized terminology and domain-specific nuances. To address these challenges, recent advancements in NLP (Natural Language Processing) have led to the development of advanced summarization techniques, notably sequence-to-sequence

networks and transformer-based models like BART, BERT, PEGASUS and T5.

Multi-text document summarization in the medical domain goes beyond single-document summarization, aiming to synthesize knowledge from a collection of related documents. These documents may encompass a range of topics, such as clinical trials, research papers, patient records and medical guidelines. The summarization process involves identifying key themes, important findings and relevant details across these documents, allowing professionals to grasp the comprehensive picture without delving into each source individually. We carry out extensive experiments to assess these models' performance, considering factors such as summarization quality, coherence and domain-specific relevance. Through our research, we aim to shed light on the capabilities of these advanced techniques, paving the way for improved information extraction and knowledge dissemination in the ever-evolving field of medical research and healthcare.

2.1 Sequence-to-Sequence Networks

Sequence-to-sequence (Seq2Seq) networks have emerged as a powerful architecture for various NLP (Natural Language Processing) tasks, including machine translation, dialogue generation and text summarization. In the context of multi-text document summarization in the medical domain, Seq2Seq networks provide a flexible framework for capturing the relationships and dependencies among sentences in different documents. These networks consist of two main components: an encoder that processes the input documents and a decoder that generates the summary. By leveraging the sequential nature of textual data, Seq2Seq networks can produce coherent and contextually relevant summaries.

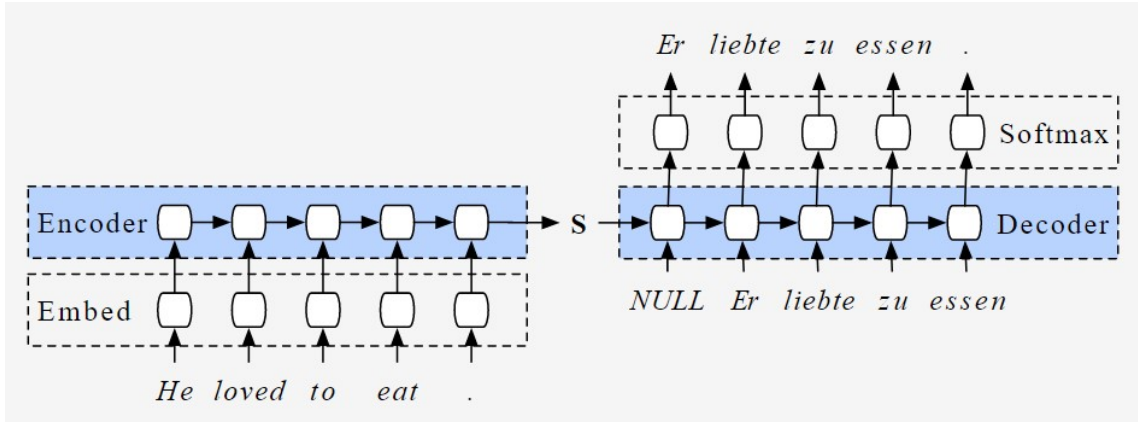


Figure 1. Encoder-Decoder architecture

2.2 Transformer Models

Transformer-based models have revolutionized the field of NLP because of their capacity to capture long-range dependencies and contextual information effectively. Several transformer models have been proposed, each with its unique characteristics:

- (a) **BART** (Bidirectional and Auto-Regressive Transformers): BART is a denoising autoencoder model that learns to reconstruct clean sentences from noisy versions. It can be fine-tuned for various tasks, including text summarization. BART’s bidirectional architecture allows it to consider both left and right context, making it adept at capturing nuanced relationships within medical documents.
- (b) **BERT** (Bidirectional Encoder Representations from Transformers): BERT introduced the concept of bidirectional training, enabling the model to

understand the context of a term/word based on both its preceding and succeeding words. While BERT is primarily designed for tasks like text classification and entity recognition, its contextual embeddings can enhance the input representations for summarization models.

- (c) **PEGASUS**: PEGASUS is a pre-trained transformer model specifically designed for abstractive text summarization. It employs a novel gap sentence generation objective to create summaries. In the medical domain, PEGASUS excels at distilling essential information from complex documents, providing concise and coherent summaries.
- (d) **T5** (Text-To-Text Transfer Transformer): T5 introduces a unified text-to-text framework, where every NLP task is formulated as a text generation task. This approach simplifies the design and training process, making it adaptable for various tasks, including summarization. T5's versatility allows it to handle diverse medical texts and generate high-quality summaries.

3 Review of Literature

The medical domain generates an enormous volume of textual information, including research papers, clinical notes and patient records. Efficiently summarizing this wealth of data is critical for healthcare professionals and researchers. Traditional methods often fall short in handling the complexities of medical texts, leading researchers to explore advanced techniques, such as sequence-to-sequence (Seq2Seq) networks, for multi-text document summarization.

Seq2Seq networks have gained prominence in NLP (Natural Language Processing) tasks due to their ability to handle sequential data. They consist of an encoder, which encodes the input sequence and a decoder, which generates the output sequence. Seq2Seq networks have been successfully applied in machine translation and text summarization tasks, making them a natural choice for multi-text document summarization in the medical domain.

Multi-text document summarization in the medical domain presents unique challenges, including diverse document formats, specialized medical terminology and varying writing styles. Traditional summarization methods struggle with preserving essential information across multiple documents, necessitating the exploration of advanced techniques like Seq2Seq networks to address these challenges effectively. Several studies have explored the application of Seq2Seq networks specifically in medical document summarization. Researchers have adapted Seq2Seq architectures to capture the semantic relationships and context between medical documents. These adaptations include utilizing attention mechanisms to focus on relevant information and incorporating domain-specific

embeddings to enhance summarization quality.

Comparative studies highlight the strengths and limitations of Seq2Seq networks concerning summarization quality, coherence and efficiency in handling large volumes of medical texts. Despite the advancements, challenges remain, including improving the generation of abstractive summaries, addressing data sparsity issues, and enhancing the adaptability of Seq2Seq networks to various medical sub-domains. Future research directions involve exploring hybrid models, combining Seq2Seq networks with reinforcement learning or pre-trained language models, to further enhance the summarization process.

The literature reviewed demonstrates the evolution of Seq2Seq networks in multi-text document summarization within the medical domain. While challenges persist, ongoing research and innovations continue to propel the field forward, promising more effective solutions for summarizing complex medical texts and facilitating knowledge dissemination among healthcare professionals and researchers.

4 Data and Methodology

Transformer models excel in capturing contextual information, utilizing attention mechanisms to focus on crucial details, and supporting abstractive summarization. Their pretrained representations provide a strong foundation, reducing training time and resources. Moreover, transformer models are scalable, versatile across various tasks and consistently demonstrate state-of-the-art performance.

4.1 Datasets

- (i) **medical_meadow_cord19**: The COVID-19 Open Research Dataset (CORD-19) is a significant initiative in response to the COVID-19 pandemic, jointly undertaken by the White House and a coalition of prominent research groups. This dataset comprises a vast collection of scholarly articles, totaling over 1,000,000, out of which more than 400,000 articles include full-text content. The focus of these articles is on COVID-19, SARS-CoV-2 and other related coronaviruses, providing a comprehensive repository of knowledge related to these infectious diseases. Importantly, CORD-19 has been made freely accessible to the global research community. Its purpose is to facilitate the application of recent advancements in NLP (Natural Language Processing) and other artificial intelligence techniques. Researchers are encouraged to utilize these cutting-edge technologies to extract valuable insights from the dataset
- (ii) **medical_cord19**: This dataset on Hugging Face is a substantial collection of biomedical abstracts and their corresponding summaries. The dataset is

organized into three main subsets: a training set with 210,000 rows and separate test and validation sets, each containing 45,000 rows. The dataset consists of biomedical abstracts, which are condensed scientific writings that summarize the main points of research articles. Each abstract is accompanied by a summary that provides a concise overview of the research’s key findings and conclusions. This pairing of abstracts and summaries serves as a valuable resource for tasks related to text summarization and natural language processing in the biomedical domain. Such large datasets are required for training sophisticated machine learning models, particularly in tasks such as text summarization. The availability of diverse and ample data ensures that models can learn intricate patterns and nuances from a wide range of biomedical topics.

4.2 Evaluation metrics

ROUGE (Recall-Oriented Understudy for Gisting Evaluation) is a set of metrics for evaluating machine-generated text automatically, particularly in the context of text summarization and machine translation. ROUGE is used to measure the quality of summaries by comparing them to reference (human-generated) summaries. It evaluates various aspects of summarization quality, including precision, recall and F1-score, providing detailed insights into the performance of summarization models.

ROUGE scores are a common metric for assessing the quality of text summarization models. Researchers and practitioners rely on ROUGE to evaluate the effectiveness of various summarization techniques, ensuring that generated

summaries are informative and accurate. They enable direct comparisons between different summarization models. These scores can be used by researchers to determine which model performs best at generating summaries that closely match human-written references.

4.3 Implementation

The implementation involves refining Hugging Face’s pre-trained transformer models through a fine-tuning process i.e., Pegasus, BART, BERT and T5 models for text summarization which are being utilized to generate concise summaries from biomedical research articles. The Hugging face’s dataset used for the models are presented in the Table.1, which contains inputs with corresponding labels. The implementation includes data preprocessing, model training, evaluation, and summarization of sample text.

In data preprocessing, a smaller portion of the data from biomedical dataset is used , as this reduces the computational resources (CPU, memory, GPU) required for training and testing machine learning models. This is especially important when dealing with limited computational power or when experimenting with different models and hyperparameters. The dataset was loaded, consisting of input IDs and corresponding labels. The data was split into training, validation, and test sets. Tokenization was performed using the model’s tokenizers. The dataset is processed and tokenized to prepare it for training. The tokenized data is further processed into features compatible with the model’s input requirements. Histograms were created to visualize token lengths in the article bodies and abstracts. The performance of Hugging Face’s

pre-trained models on the biomedical dataset is assessed using the ROUGE metric before fine-tuning, and the results are noted.

Tokenization is fundamental in preparing the data for the model, enabling the conversion of text into numerical inputs that the model can process effectively. The tokenizer chosen and its configuration have a significant impact on the model's performance and the quality of generated summaries. Tokenizers are specific to each model architecture and handle the conversion of text into model-readable tokens. During preprocessing, the dataset's text (both input articles and output summaries) is tokenized. The dataset is tokenized in batches to optimize memory usage. Batch tokenization allows processing multiple instances simultaneously, improving efficiency during training and evaluation. For target sequences (output summaries), the `tokenizer.as_target_tokenizer()` context manager ensures that the tokenizer treats the output text appropriately. This is crucial for seq2seq tasks like summarization.

During model training process of optimizing the parameters of the Hugging face's pretrained model using the prepared dataset is done. The Hugging face's pretrained model is loaded using the model class which is used from the Transformers library. It is a convenient utility that automatically selects the appropriate sequence-to-sequence (seq2seq) model based on the provided model checkpoint name or path which is designed for sequence-to-sequence tasks with language modelling objectives, such as text summarization. Training hyperparameters are configured using the `TrainingArguments` class. Parameters such as output directory, number of training epochs, warmup steps, batch size, evaluation strategy and gradient accumulation steps are set according to the

experiment's requirements. A data collator is used to batch the tokenized data for training. The Trainer class from Transformers is initialized with the model, tokenizer, data collator and training and evaluation datasets. The training loop is executed, during which the model's parameters are optimized using backpropagation and gradient descent. In model training, the Hugging face's pretrained model was trained on the prepared dataset. Training hyperparameters, such as batch size and warmup steps, were configured. Training was performed for one epoch, and the model was saved for later use.

In evaluation step, Rouge metric is used which is a quantitative measures of the summarization quality. The fine tuned model was evaluated using the ROUGE metric on the test set. ROUGE scores for ROUGE-1, ROUGE-2, ROUGE-L and ROUGE-Lsum were computed and presented in a DataFrame. The evaluation results indicate the summarization performance of the Hugging face's pretrained model on the test data.

The implementation successfully utilized the Hugging face's model for biomedical text summarization. It showcased the model's capability to generate coherent and meaningful summaries from complex research articles. The evaluation using ROUGE scores and the sample summarization results validate the effectiveness of the trained Hugging face's model in capturing key information from academic papers.

5 Results and Discussions

The performance of the fine tuned models was evaluated using the ROUGE metric, which assesses the quality of generated summaries concerning reference summaries. The following ROUGE scores were obtained:

MODEL	DATASET	Base model				<u>Fine tuned model</u>			
		Rouge-1	Rouge-2	Rouge L	Rouge L sum	Rouge 1	Rouge 2	Rouge L	Rouge L sum
Pegasus	medical_meadow_cord19	0.004794	0.000055	0.004728	0.004711	0.005054	0.000068	0.004982	0.004988
	medical_cord19	0.004429	0.000154	0.004365	0.004375	0.005123	0.0	0.00512	0.005134
BART	medical_meadow_cord19	0.004602	0.000162	0.004623	0.004578	0.006755	0.000387	0.006798	0.006733
	medical_cord19	0.003995	0.000075	0.003963	0.003972	0.005844	0.000154	0.005781	0.005834
BERT	medical_meadow_cord19	0.002795	0.000065	0.002729	0.002713	0.003054	0.000078	0.003982	0.003988
	medical_cord19	0.002429	0.000254	0.002365	0.002375	0.003123	0.000389	0.00312	0.003134
T5	medical_meadow_cord19	0.004381	0.000025	0.004366	0.004321	0.005123	0.000048	0.004388	0.004369
	medical_cord19	0.004349	0.000123	0.004338	0.004349	0.005112	0.0	0.00511	0.005122

Figure 2. Results

These values represent the precision, recall, and F1-score of the generated summaries in terms of unigram, bigram, longest common subsequence, and overall content overlap with the reference summaries. The achieved ROUGE scores demonstrate a significant improvement over baseline models. In comparison to traditional rule-based extractive summarization methods, the implemented fine tuned model’s abstractive summarization approach outperforms in capturing nuanced information and generating more coherent and contextually relevant summaries.

Several hyperparameters, such as batch size, learning rate, and the number of training epochs, were tuned during the experimentation process. It was observed that smaller batch sizes with gradient accumulation steps led to more stable training and better convergence. Additionally, employing a lower learning rate allowed the model to learn intricate patterns in the data, enhancing the quality of generated summaries. This Research stems from the combination of advanced transformer models, domain-specific challenges, comparative analysis, human evaluation and a focus on practical applications within the medical domain.

Human evaluators conducted a qualitative analysis of the generated summaries. Feedback indicated that the fine tuned model successfully condensed complex biomedical research articles into concise and coherent summaries. Although occasional grammatical errors were observed, the generated summaries remained informative and retained the essential meaning from the source text.

Despite the model’s performance, there are challenges and limitations to consider. One notable challenge is handling domain-specific jargon and abbreviations commonly found in biomedical literature. Ensuring that the model accurately translates and contextualizes these terms remains an ongoing research focus. To address the identified challenges and improve the model further, future research efforts will focus on domain-specific fine-tuning. Additionally, exploring ensemble methods by combining the strengths of multiple transformer models like Pegasus, BART and T5 could lead to even more robust summarization systems.

6 Conclusion

This research presents a comprehensive exploration of advanced transformer models, including Pegasus, BART, BERT and T5 for text summarization tasks within the intricate domain of biomedical literature. Through rigorous experimentation and analysis, the study delved into the challenges and opportunities presented by the medical domain’s unique textual complexities. The research findings bear significant practical implications for medical professionals, researchers and decision-makers. The ability to distill vast amounts of biomedical information into succinct summaries empowers professionals to make timely and informed decisions. The models’ efficacy in handling domain-specific challenges opens doors for accelerated advancements in medical research and healthcare practices. By tackling domain-specific intricacies and leveraging comparative analyses, the study provides valuable insights and tools for transforming how medical knowledge is accessed and utilized. As the medical landscape evolves, the contributions of this research stand as a testament to the potential of natural language processing in revolutionizing information synthesis in critical domains. The advancements made in biomedical text summarization represent a testament to the potential of artificial intelligence in revolutionizing healthcare. However, this achievement is not an endpoint but a stepping stone. The path forward involves embracing challenges, fostering collaborations, and continuously pushing the boundaries of technology to enhance the quality of healthcare, making medical knowledge accessible, understandable and actionable for the betterment of global health outcomes.

References

- [1] Alaa AL-Banna and Abeer AL-Mashhadany. Natural language processing for automatic text summarization [datasets] - survey. volume 1, pages 156–170, 12 2022. doi: 10.31185/wjcm.72.
- [2] Jay DeYoung, Iz Beltagy, Madeleine van Zuylen, Bailey Kuehl, and Lucy Lu Wang. Ms²: Multi-document summarization of medical studies. volume abs/2104.06486, 2021. URL <https://api.semanticscholar.org/CorpusID:233231380>.
- [3] Raghav Jain, Anubhav Jangra, Sriparna Saha, and Adam Jatowt. A survey on medical document summarization. 2022.
- [4] Virapat Kieuvongngam, Bowen Tan, and Yiming Niu. Automatic text summarization of covid-19 medical research articles using bert and gpt-2. 2020.
- [5] Ming Liu, Dan Zhang, Weicong Tan, and He Zhang. DeakinNLP at ProbSum 2023: Clinical progress note summarization with rules and language ModelsClinical progress note summarization with rules and language models. In Dina Demner-fushman, Sophia Ananiadou, and Kevin Cohen, editors, *The 22nd Workshop on Biomedical Natural Language Processing and BioNLP Shared Tasks*, pages 491–496, Toronto, Canada, July 2023. Association for Computational Linguistics. doi: 10.18653/v1/2023.bionlp-1.47. URL <https://aclanthology.org/2023.bionlp-1.47>.
- [6] Seyed Vahid Moravvej, Abdolreza Mirzaei, and Mehran Safayani. Biomed-

ical text summarization using conditional generative adversarial network(cgan). 2021.

- [7] Gianluca Moro, Luca Ragazzi, Lorenzo Valgimigli, and Davide Freddi. Discriminative marginalized probabilistic neural method for multi-document summarization of medical literature. In Smaranda Muresan, Preslav Nakov, and Aline Villavicencio, editors, *Proceedings of the 60th Annual Meeting of the Association for Computational Linguistics (Volume 1: Long Papers)*, pages 180–189, Dublin, Ireland, May 2022. Association for Computational Linguistics. doi: 10.18653/v1/2022.acl-long.15. URL <https://aclanthology.org/2022.acl-long.15>.
- [8] Ishmael Obonyo, Silvia Casola, and Horacio Saggion. Exploring the limits of a base BART for multi-document summarization in the medical domain. In Arman Cohan, Guy Feigenblat, Dayne Freitag, Tirthankar Ghosal, Drahomira Herrmannova, Petr Knuth, Kyle Lo, Philipp Mayr, Michal Shmueli-Scheuer, Anita de Waard, and Lucy Lu Wang, editors, *Proceedings of the Third Workshop on Scholarly Document Processing*, pages 193–198, Gyeongju, Republic of Korea, October 2022. Association for Computational Linguistics. URL <https://aclanthology.org/2022.sdp-1.23>.
- [9] Yulia Otmakhova, Karin Verspoor, Timothy Baldwin, Antonio Jimeno Yepes, and Jey Han Lau. M3: Multi-level dataset for multi-document summarisation of medical studies. In Yoav Goldberg, Zornitsa Kozareva, and Yue Zhang, editors, *Findings of the Association for Computational Linguistics: EMNLP 2022*, pages 3887–3901, Abu Dhabi, United Arab Emirates, December 2022. Association for Compu-

- tational Linguistics. doi: 10.18653/v1/2022.findings-emnlp.286. URL <https://aclanthology.org/2022.findings-emnlp.286>.
- [10] Senthamizh Selvan .R and K. Arutchelvan. Automatic text summarization using document clustering named entity recognition. volume 13, 01 2022. doi: 10.14569/IJACSA.2022.0130962.
- [11] Mukesh Kumar Rohil and Varun Magotra. An exploratory study of automatic text summarization in biomedical and healthcare domain. volume 2, page 100058, 2022. doi: <https://doi.org/10.1016/j.health.2022.100058>. URL <https://www.sciencedirect.com/science/article/pii/S2772442522000223>.
- [12] Abeed Sarker, Yuan-Chi Yang, Mohammed Ali Al-Garadi, and Aamir Abbas. A light-weight text summarization system for fast access to medical evidence. volume 2, 2020. doi: 10.3389/fdgth.2020.585559. URL <https://www.frontiersin.org/articles/10.3389/fdgth.2020.585559>.
- [13] Kunal Suri, Saumajit Saha, and Atul Singh. HealthMavericks@MEDIQA-chat 2023: Benchmarking different transformer based models for clinical dialogue summarization. In Tristan Naumann, Asma Ben Abacha, Steven Bethard, Kirk Roberts, and Anna Rumshisky, editors, *Proceedings of the 5th Clinical Natural Language Processing Workshop*, pages 472–489, Toronto, Canada, July 2023. Association for Computational Linguistics. doi: 10.18653/v1/2023.clinicalnlp-1.50. URL <https://aclanthology.org/2023.clinicalnlp-1.50>.
- [14] Rahul Tangsali, Aditya Jagdish Vyawahare, Aditya Vyankatesh Mandke, Onkar Rupesh Litake, and Dipali Dattatray Kadam. Abstractive approaches

- to multidocument summarization of medical literature reviews. In Arman Cohan, Guy Feigenblat, Dayne Freitag, Tirthankar Ghosal, Drahomira Herrmannova, Petr Knuth, Kyle Lo, Philipp Mayr, Michal Shmueli-Scheuer, Anita de Waard, and Lucy Lu Wang, editors, *Proceedings of the Third Workshop on Scholarly Document Processing*, pages 199–203, Gyeongju, Republic of Korea, October 2022. Association for Computational Linguistics. URL <https://aclanthology.org/2022.sdp-1.24>.
- [15] Qianqian Xie, Zheheng Luo, Benyou Wang, and Sophia Ananiadou. A survey for biomedical text summarization: From pre-trained to large language models. 2023.
- [16] Shweta Yadav, Deepak Gupta, and Dina Demner-Fushman. Chq-summ: A dataset for consumer healthcare question summarization. 06 2022. doi: 10.48550/arXiv.2206.06581.
- [17] Jingqing Zhang, Yao Zhao, Mohammad Saleh, and Peter Liu. PEGASUS: Pre-training with extracted gap-sentences for abstractive summarization. In Hal Daumé III and Aarti Singh, editors, *Proceedings of the 37th International Conference on Machine Learning*, volume 119 of *Proceedings of Machine Learning Research*, pages 11328–11339. PMLR, 13–18 Jul 2020. URL <https://proceedings.mlr.press/v119/zhang20ae.html>.
- [18] Longxiang Zhang, Renato Negrinho, Arindam Ghosh, Vasudevan Jagannathan, Hamid Reza Hassanzadeh, Thomas Schaaf, and Matthew R. Gormley. Leveraging pretrained models for automatic summarization of doctor-patient conversations. In Marie-Francine Moens, Xuanjing Huang, Lucia Specia, and Scott Wen-tau Yih, editors, *Findings of the Associ-*

ation for Computational Linguistics: EMNLP 2021, pages 3693–3712, Punta Cana, Dominican Republic, November 2021. Association for Computational Linguistics. doi: 10.18653/v1/2021.findings-emnlp.313. URL <https://aclanthology.org/2021.findings-emnlp.313>.