





# Neural reranking

Georgios Peikos, Wojciech Kusa, Annisa Maulida Ningtyas, Oscar E. Mendoza

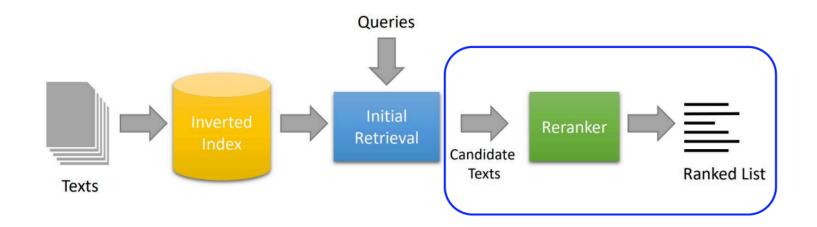
- 1. Neural retrieval recap
- 2. Challenges in medical neural retrieval
- 3. Neural retrieval for clinical trials
- 4. Introduction to the TCRR model
- 5. Performance tracking
- 6. Hands-on #1: model training
- 7. Hands-on #2: inference



- 1. Neural retrieval recap
- 2. Challenges in medical neural retrieval
- 3. Neural retrieval for clinical trials
- 4. Introduction to the TCRR model
- 5. Performance tracking
- 6. Hands-on #1: model training
- 7. Hands-on #2: inference



## **Neural Retrieval**



## Three approaches to neural IR

- 1. Cross-encoder
- 2. Bi-encoder
- 3. Learned sparse retrieval

- 1. Neural retrieval recap
- 2. Challenges in medical neural retrieval
- 3. Neural retrieval for clinical trials
- 4. Introduction to the TCRR model
- 5. Performance tracking
- 6. Hands-on #1: model training
- 7. Hands-on #2: inference



## **Technical Challenges**

- Data Quality
- Interpretability
- Scalability
- Integration

## **Ethical and Regulatory Challenges**

- Patient Privacy
- Bias and Fairness
- Regulatory Hurdles
- Accountability

#### BigBio



Figure 2: Treemap visualization of BIGBIO's 126 datasets and 13 task categories, denoted by color.

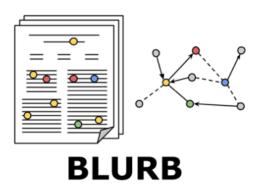
## **BIGBIO: A Framework for Data-Centric Biomedical Natural Language Processing**

Jason Alan Fries<sup>1\*</sup> Leon Weber<sup>2,3\*</sup> Natasha Seelam<sup>4\*</sup> Gabriel Altay<sup>5\*</sup> Debajyoti Datta<sup>6†</sup> Ruisi Su<sup>7†</sup> Samuele Garda<sup>2†</sup> Sunny MS Kang<sup>8†</sup> Stella Biderman<sup>9,10†</sup> Matthias Samwald<sup>11†</sup> Stephen H. Bach<sup>12†</sup> Wojciech Kusa<sup>13†</sup> Samuel Cahyawijava<sup>14†</sup> Fabio Barth<sup>2†</sup> Simon Ott<sup>11†</sup> Mario Sänger<sup>2†</sup> Bo Wang<sup>15</sup> Alison Callahan<sup>1</sup> Daniel León Periñán<sup>16</sup> Théo Gigant<sup>7</sup> Patrick Haller<sup>2</sup> Jenny Chim<sup>17</sup> Jose Posada<sup>18</sup> John Giorgi<sup>19</sup> Karthik Rangasai Siyaraman<sup>20</sup> Marc Pàmies<sup>21</sup> Marianna Nezhurina<sup>22</sup> Robert Martin<sup>2</sup> Moritz Freidank<sup>23</sup> Nathan Dahlberg<sup>7</sup> Shubhanshu Mishra<sup>24</sup> Shamik Bose<sup>7</sup> Nicholas Broad<sup>25</sup> Yanis Labrak<sup>26</sup> Shlok S Deshmukh<sup>27</sup> Sid Kiblawi<sup>28</sup> Ayush Singh<sup>7</sup> Minh Chien Vu<sup>29</sup> Trishala Neeraj<sup>30</sup> Jonas Golde<sup>2</sup> Albert Villanova del Moral<sup>25</sup> Benjamin Beilharz<sup>31</sup> <sup>1</sup>Stanford University <sup>2</sup>Humboldt-Universität zu Berlin <sup>3</sup>Max Delbrück Center for Molecular Medicine <sup>4</sup>Sherlock Biosciences <sup>5</sup>Tempus Labs Inc. <sup>6</sup>University of Virginia <sup>7</sup>BigScience <sup>8</sup>Immuneering <sup>9</sup>EleutherAI <sup>10</sup>Booz Allen Hamilton <sup>11</sup>Institute of Artificial Intelligence, Medical University of Vienna <sup>12</sup>Brown University <sup>13</sup>TU Wien <sup>14</sup>The Hong Kong University of Science and Technology <sup>15-31</sup>See Appendix B \*Equal Contribution †Equal Contribution Corresponding Authors: jason-fries@stanford.edu leonweber@posteo.de nseelam1@gmail.com gabriel.altav@gmail.com

- BigBio
- BLURB

## Domain-Specific Language Model Pretraining for Biomedical Natural Language Processing

YU GU\*, ROBERT TINN\*, HAO CHENG\*, MICHAEL LUCAS, NAOTO USUYAMA, XIAODONG LIU, TRISTAN NAUMANN, JIANFENG GAO, and HOIFUNG POON, Microsoft Research



- BigBio
- BLURB
- CBLUE

#### CBLUE: A Chinese Biomedical Language Understanding Evaluation Benchmark

Ningyu Zhang<sup>1</sup>\*, Mosha Chen<sup>2</sup>\*, Zhen Bi<sup>1</sup>\*, Xiaozhuan Liang<sup>1</sup>\*, Lei Li<sup>1</sup>\*, Xin Shang<sup>3</sup>
Kangping Yin<sup>2</sup>, Chuanqi Tan<sup>2</sup>, Jian Xu<sup>2</sup>, Fei Huang<sup>2</sup>, Luo Si<sup>2</sup>, Yuan Ni<sup>4</sup>, Guotong Xie<sup>4,5,6</sup>
Zhifang Sui<sup>7,13</sup>, Baobao Chang<sup>7,13</sup>, Hui Zong<sup>8,14</sup>, Zheng Yuan<sup>9</sup>, Linfeng Li<sup>10</sup>, Jun Yan<sup>10</sup>
Hongying Zan<sup>11,13</sup>, Kunli Zhang<sup>11,13</sup>, Buzhou Tang<sup>12,13</sup>†, Qingcai Chen<sup>12,13</sup>†

<sup>1</sup>Alibaba-Zhejiang University Joint Research Institute of Frontier Technologies, Zhejiang University

<sup>2</sup>Alibaba Group, <sup>3</sup>School of Mathematical Science, Zhejiang University, <sup>4</sup>Pingan Health Technology

<sup>5</sup>Ping An Health Cloud Company Limited <sup>6</sup>Ping An International Smart City Technology Co., Ltd

<sup>7</sup>Key Laboratory of Computational Linguistics, Ministry of Education, Peking University

<sup>8</sup>School of Life Sciences and Technology, Tongji University <sup>9</sup>Tsinghua University,

<sup>10</sup>Yidu Cloud Technology Inc <sup>11</sup>School of Information Engineering, Zhengzhou University

<sup>12</sup>Harbin Institute of Technology (Shenzhen) <sup>13</sup>Peng Cheng Laboratory, <sup>14</sup>Philips Research China

- BigBio
- BLURB
- CBLUE
- https://ir-datasets.com

# ir\_datasets: Catalog ir\_datasets provides a common interface to many IR ranking datasets. Getting Started Install with pip: pip install --upgrade ir\_datasets

## Medical models

- BioBERT
- SciBERT
- BlueBERT
- ClinicalBERT

- ClinicalLongformer
- ClinicalBigBird
- ...

- 1. Neural retrieval recap
- 2. Challenges in medical neural retrieval
- 3. Neural retrieval for clinical trials
- 4. Introduction to the TCRR model
- 5. Performance tracking
- 6. Hands-on #1: model training
- 7. Hands-on #2: inference

## Neural retrieval for clinical trials

- 1. Neural query expansion with T5
- 2. Dense retrieval
- 3. Cross encoder

Neural Query Synthesis and Domain-Specific Ranking
Templates for Multi-Stage Clinical Trial Matching

Authors: Ronak Pradeep, Yilin Li, Yuetong Wang, Jimmy Lin Authors Info & Claims

SIGIR '22: Proceedings of the 45th International ACM SIGIR Conference on Research and Development in Information Retrieval • July 2022 • Pages 2325–2330 • https://doi.org/10.1145/3477495.3531853

Published: 07 July 2022 Publication History

A Check for updates

#### **■ ABSTRACT**

In this work, we propose an effective multi-stage neural ranking system for the clinical trial matching problem. First, we introduce NQS, a neural query synthesis method that leverages a zero-shot document expansion model to generate multiple sentence-long queries from lengthy patient descriptions. These queries are independently issued to a search engine and the results are fused. We find that on the TREC 2021 Clinical Trials Track, this method outperforms strong traditional baselines like BM25 and BM25 + RM3 by about 12 points in nDCG@10, a relative improvement of 34%. This simple method is so effective that even a state-of-the-art neural relevance ranking method trained on the medical subset of MS MARCO passage, when reranking the results of NQS, fails to improve on the ranked list. Second, we introduce a two-stage neural reranking pipeline trained on clinical trial matching data using tailored ranking templates. In this setting, we can train a pointwise reranker using just 1.1k positive examples and obtain effectiveness improvements over NQS by 24 points. This end-to-end multi-stage system demonstrates a 20% relative effectiveness gain compared to the second-best submission at TREC 2021, making it an important step towards better automated clinical trial matching.





#### Journal of Biomedical Informatics

Volume 144, August 2023, 104444



## Effective matching of patients to clinical trials using entity extraction and neural re-ranking

#### Highlights

- We conduct several experiments for the patient-to-trial matching retrieval problem.
- Inclusion criteria section has the biggest influence on the score in lexical models.
- Query and document enrichment techniques improve retrieval of relevant trials.
- Age and gender-based filtering helped remove 26% ineligible trials.
- Novel training strategy for re-ranking further increases retrieval effectiveness.



#### Matching a Patient from An Admission Note to Clinical Trials: Experiments with Query Generation and Neural-Ranking

Vincent Nguyen Maciej Rybinski Sarvnaz Karimi CSIRO Data61 Sydney, Australia firstname.lastname@csiro.au

#### ABSTRACT

Many clinical trials fail to attract enough eligible participants. The TREC 2022 Clinical Trials track set a task where patient data, in the form of clinical notes, can be used to match eligible patients to a relevant clinical trial. We explore a number of dense retrieval methods using Bidirectional Encoder Representations from Transformers (BERT). Our best method used BERT reranking using models based on monoBERT architecture. Our self-supervised monoBERT run achieved effectiveness competitive to that of a fully-tuned monoBERT run.

#### CCS CONCEPTS

Information systems → Retrieval models and ranking;
 Language models; Decision support systems;
 Applied computing → Health informatics.

#### KEYWORDS

Clinical trials search; Medical information retrieval; Learningto-rank; Evidence-based medicine

#### ACM Reference Format:

Vincent Nguyen Maciej Rybinski Sarvnaz Karimi. 2021. Matching a Patient from An Admission Note to Clinical Trials: Experiments with Query Generation and Neural-Ranking. In TREC'22: TREC, November, 2022. ACM, New York, NY, USA, 4 pages. tasks [4–6] in its 2017, 2018, and 2019 editions. The task of this year's track is to link a synthetic patient's electronic health record (EHR), in free text, to relevant clinical trials. TREC CT's goal is to study the use of automatic retrieval systems to expose patients to relevant clinical trials to increase participation.

In our submission to this year in the TREC CT track, we build upon our last year's submission [7]. Our experiments this year focus on neural ranking using resource-effective self-supervision and supervision signals from last year's judgement pool. Our experiments with a neural reranking pipeline centered around resource-effective learning, used a reranker trained on labeled data (from last year's edition of the track) compared with a self-supervised model trained using the target document corpus. We also experiment with efficient end-to-end neural ranking (where document representations can be pre-computed) with bi-encoders and with neural query expansion. Finally, we also probe the effect of a simple heuristic for matching the patient note with the demographic profile specified in the clinical trials, which we apply to one of the bi-encoder runs.

#### 2 DATASET

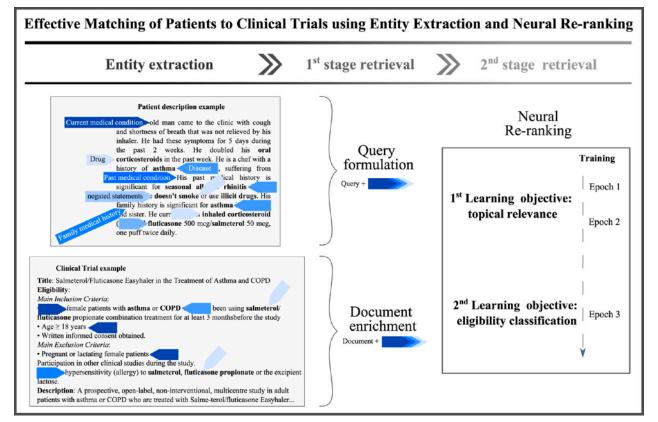
The TREC 2022 CT dataset consists of 50 topics with 35,394



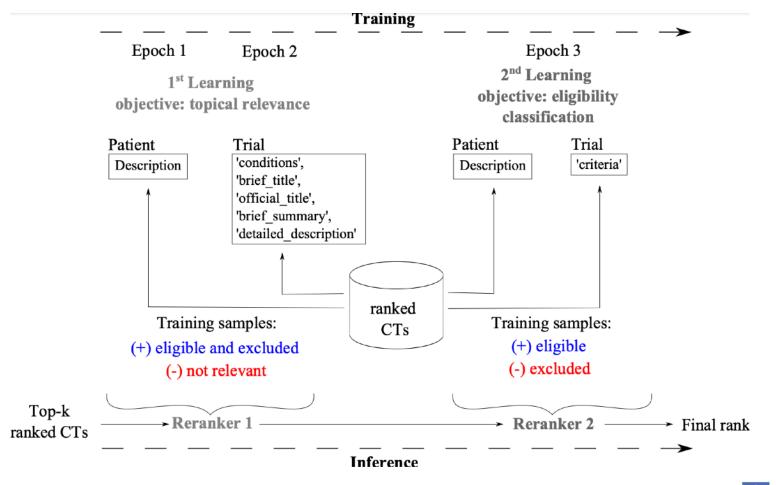
- 1. Neural retrieval recap
- 2. Challenges in medical neural retrieval
- 3. Neural retrieval for clinical trials
- 4. Introduction to the TCRR model
- 5. Performance tracking
- 6. Hands-on #1: model training
- 7. Hands-on #2: inference

## Topical and Criteria Re-Ranking — TCRR





# Training Pipeline



- 1. Neural retrieval recap
- 2. Challenges in medical neural retrieval
- 3. Neural retrieval for clinical trials
- 4. Introduction to the TCRR model
- 5. Performance tracking
- 6. Hands-on #1: model training
- 7. Hands-on #2: inference



## What can be visualised?

- 1. Model architecture
- 2. Model training
- 3. Model inference

## What can be visualised?

- 1. Model architecture
- 2. Model training
- 3. Model inference

## Wandb example

```
# train.py
import wandb
import random # for demo script
wandb.login()
epochs=10
lr=0.01
run = wandb.init(
    # Set the project where this run will be logged
    project="my-awesome-project",
    # Track hyperparameters and run metadata
    config={
        "learning_rate": lr,
        "epochs": epochs,
   })
offset = random.random() / 5
print(f"lr: {lr}")
# simulating a training run
for epoch in range(2, epochs):
    acc = 1 - 2 ** -epoch - random.random() / epoch -
offsets = 2 ** -epoch + random.random() / epoch + offset
    print(f"epoch={epoch}, accuracy={acc}, loss={loss}")
    wandb.log({"accuracy": acc, "loss": loss})
# run.log code()
```

# Wandb — PyTorch example

```
import wandb
wandb.init(config=args)
# set up your model
model = AutoModelForSequenceClassification.from_pretrained(
               model_name, num_labels=2
# Magic
wandb.watch(model, log_freq=100)
model.train()
for batch_idx, (data, target) in enumerate(train_loader):
    output = model(data)
    loss = F.nll_loss(output, target)
    loss.backward()
    optimizer.step()
    if batch_idx % args.log_interval == 0:
        wandb.log({"loss": loss})
```

## Wandb — logging metrics

```
predictions = trainer.predict(
   tokenized_datasets[test_data],
wandb.log(
       f"{test_data}_precision": predictions.metrics["test_precision"],
        f"{test_data}_recall": predictions.metrics["test_recall"],
       f"{test_data}_f1": predictions.metrics["test_f1"],
       f"{test_data}_loss": predictions.metrics["test_loss"],
```

- 1. Neural retrieval recap
- 2. Challenges in medical neural retrieval
- 3. Neural retrieval for clinical trials
- 4. Introduction to the TCRR model
- 5. Performance tracking
- 6. Hands-on #1: model training
- 7. Hands-on #2: inference



## Hands-on Session 1: Training with TCRR

Google Colab

- 1. Neural retrieval recap
- 2. Challenges in medical neural retrieval
- 3. Neural retrieval for clinical trials
- 4. Introduction to the TCRR model
- 5. Performance tracking
- 6. Hands-on #1: model training
- 7. Hands-on #2: inference

## Hands-on Session 2: Inference and Application

Google Colab



## **Questions?**