

Облегчение моделей by design

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AGENDA

Machine Reading Comprehension

Retrieval to the rescue

O3 Entity Linking

01

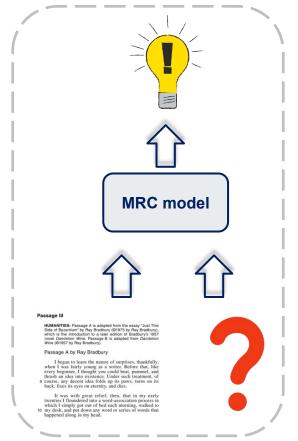
Machine Reading Comprehension

Machine Reading Comprehension (MRC) as Explainability by initio

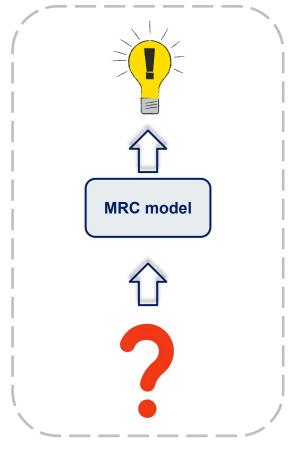
- Question Answering (QA): standard NLP task
- Now most of the best QA-systems are generation-based:
 - Means that only large (or even HUGE) decoder is used
 - All the information needed to answer the question is stored inside decoder weights
 - But the output is unexplainable: the model just knows (or not!) the answer
- What we'd like to have: the explainability WHY the system provides this answer
- In terms of MRC it means that the system can provide the relevant text passage (or passages), containing the correct answer
 - And the human can understand whether the system was right about it's guessing
 - At the same time, it can lead to decreasing the model size (usage of a number of small models
 is still more efficient than one huge decoder)



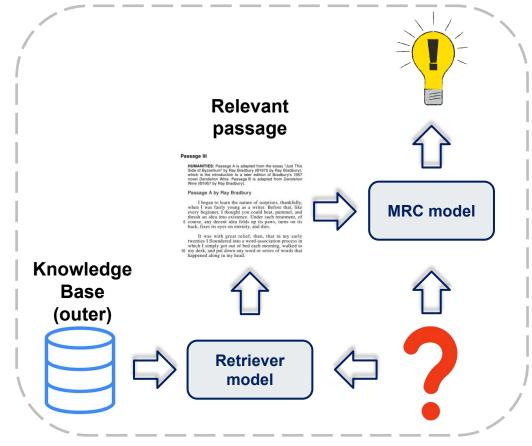
Machine Reading Comprehension: common paradigms



Extraction of knowledge from relevant passage Not possible in real-world



Generation of knowledge^{1,2}
Not scalable, all information
is stored inside MRC
model weights (like T5/GPT-3)



2-stage: <u>first</u> to <u>retrieve</u> the relevant model from outer text corpus, <u>then extract</u> knowledge from this passage

Realistic, explainable and scalable approach

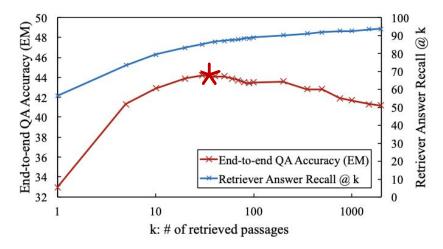


02

Retrieval to the rescue!

Retriever ≠ Reader¹

(a) End-to-end QA accuracy (Exact Match, y-axis on the left) of DPR reader and the retrieval recall rate (y-axis on the right) of DPR retriever.



$$p_{\eta}(z|x) \propto \exp\left(\mathbf{d}(z)^{\top}\mathbf{q}(x)\right)$$

 $\mathbf{d}(z) = \mathsf{BERT}_d(z), \ \mathbf{q}(x) = \mathsf{BERT}_q(x)$

BERT as a Retriever (DPR)

Main idea:

- Retriever is not approx. of Reader: having more data helps a little for the Reader, but then drops quickly
- Retriever is a sort of <u>representational bottleneck</u>
- Can improve Retriever by KD from Reader: helps significantly for retrieval, but not so much for MRC
 - RDR: Reader-distilled Retriever
- KD by aligning similarities doc <> query

Retriever improvement after KD

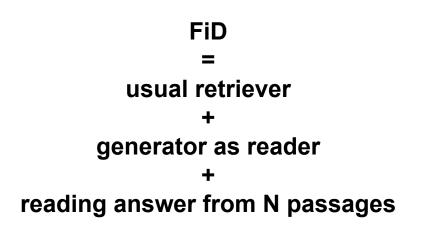
| Dataset | NQ-dev | | | NQ-test | | | | TriviaQA-test | | | | |
|------------|--------------------------------------|--------------------------------------|-------------------|-------------------------------|------|--------------------------------------|------|--------------------------------------|------|--------------------------------------|-------------------------------|--|
| Top-k | 1 | 20 | 50 | 100 | 1 | 20 | 50 | 100 | 1 | 20 | 50 | 100 |
| DPR-Single | 44.2 [‡] 54.1 (+9.9) | 76.9 [‡] 80.7 (+3.8) | 84.1 | 84.2 85.8 (+1.6) | 54.2 | 78.4 [†] 82.8 (+4.4) | 86.3 | 85.4 [†] 88.2 (+2.8) | 62.5 | 79.4 [†] 82.5 (+3.1) | 82.9 85.7 (+2.8) | 85.0 [†] 87.3 (+2.3) |
| SOTA | 51.7‡ | 79.2 [‡] | 83.0 [‡] | - | - | 79.4 [†] | -1 | 86.0^{\dagger} | - | 79.9 [†] | 1- | 85.0 [†] |

Reader improvement after KD

| Dataset | | NQ-test | | TriviaQA-test | | | |
|------------|---------------------|---------------------|----------|---------------------|---------------------|----------|--|
| | Top-1 | Report | ed | Top-1 | Reported | | |
| <u>-</u> | EM | EM | Top-k | EM | EM | Top-k | |
| DPR-Single | 32.3 37.3 (+5.0) | 41.5 42.1 (+0.6) | 50 10 | 44.5 49.1 (+4.6) | 56.8 57.0 (+0.2) | 50 50 | |
| RAG-Token | 39.4 40.9 (+1.5) | 44.1 44.5 (+0.4) | 15 15 | - | 55.2 | - | |



Fusion-in-Decoder (FiD)¹: RB model for MRC



Main idea:

- Retriever: DPR (BERT-doc + BERT-query)
- Reader is seq2seq T5, having query + retrieved doc as an input
 - added special tokens question:, title: and context:
 before the question, title and text of each passage
- Fusion-in-Decoder: output based on N > 1 passages

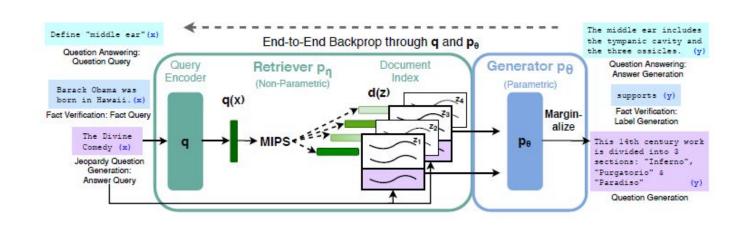


Retrieval-Augmented Generation (RAG)¹: RB model for MRC

RAG = usual retriever + generator as reader

Main idea:

- End-to-end backprop through retriever AND reader
- **Retriever** is initialized from **DPR**² approach
- Reader is seq2seq BART, having query + retrieved doc as an input
- Generator can provide the output based on 1 passage (Sequence-based) or k > 1 passages (Token-based)
- Better than BERT-based reader, but more heavy (400M vs 110M)



Seq2seq generator (BART) As a Reader

1 passage:
$$p_{\text{RAG-Sequence}}(y|x) \approx \sum_{z \in \text{top-}k(p(\cdot|x))} p_{\eta}(z|x) \prod_{i}^{N} p_{\theta}(y_{i}|x,z,y_{1:i-1})$$

k passages:
$$p_{\text{RAG-Token}}(y|x) \approx \prod_{i}^{N} \sum_{z \in \text{top-}k(p(\cdot|x))} p_{\eta}(z|x) p_{\theta}(y_{i}|x,z,y_{1:i-1})$$



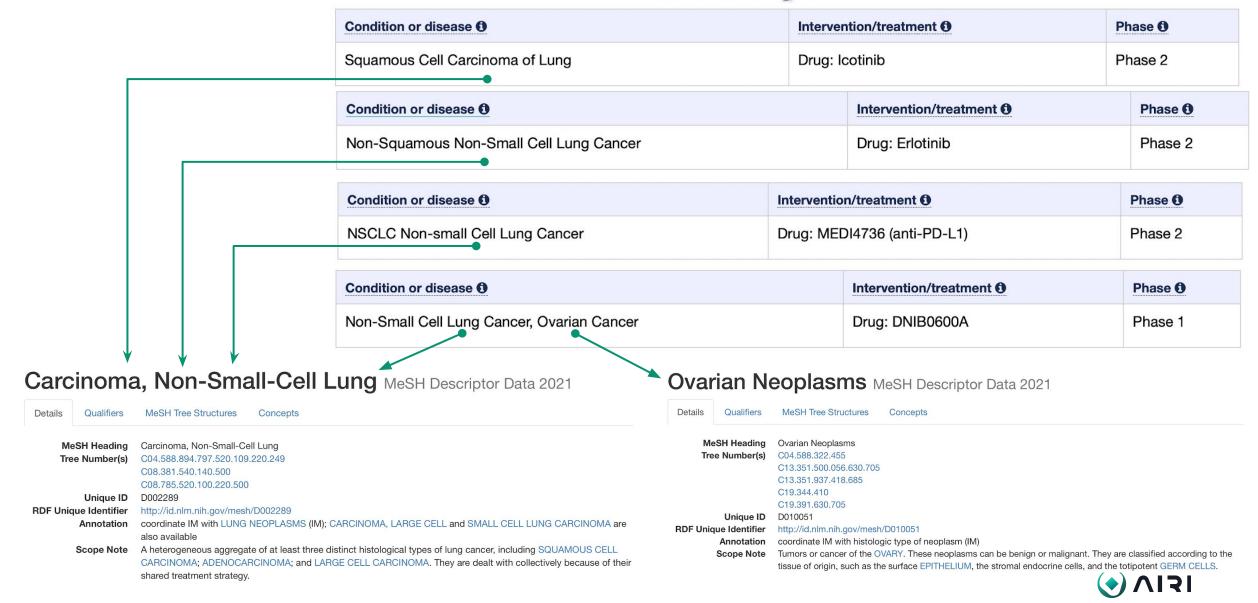
03

Entity Linking

Biomedical Entity Linking

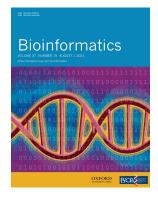


Clinical Trials.gov









Our approach DILBERT

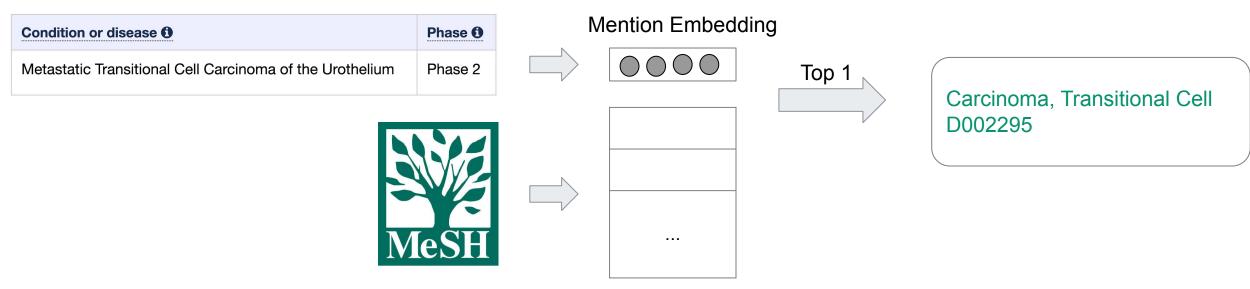
Drug and Disease Interpretation Learning with Biomedical Entity Representation Transformer

Zulfat Miftahutdinov, Artur Kadurin, Roman Kudrin, Elena Tutubalina



DILBERT - Design

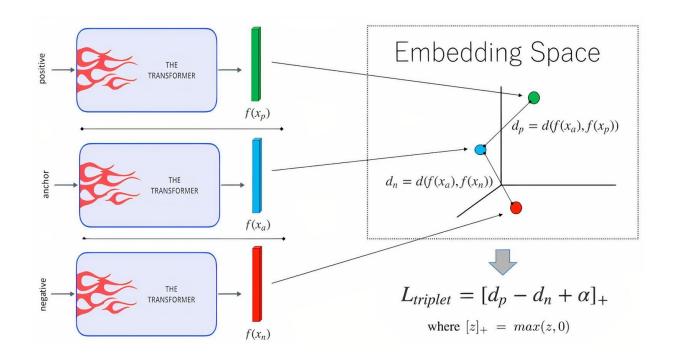
- Most of the best biomedical entity linking systems:
 - are trained & evaluated in the single-terminology setting
 - use classification type losses and online processing (a.k.a. readers)
- We focus on cross-terminology mapping of entity mentions to a given lexicon without additional re-training
- Fast, real-time inference -- all concept names from a terminology are cached





DILBERT - Training

 We use triplets of free-form entity mention, positive and negative concept names



Disease mention

| Condition or disease 1 | Phase 1 |
|----------------------------------|---------|
| NSCLC Non-small Cell Lung Cancer | Phase 2 |

Positive concept names

Carcinoma, Non-Small-Cell Lung
Non-Small Cell Lung Cancer
Non-Small Cell Lung Carcinoma

The rest of the MeSH dictionary for negative sampling

Carcinoma, Bronchogenic

Lung Neoplasms

Cancer of the Lung

Rhinitis

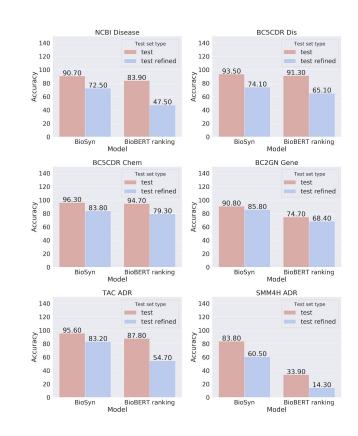
Let's remove bias!



Fair Evaluation in Concept Normalization: a Large-scale Comparative Analysis for BERT-based Models

Elena Tutubalina, Artur Kadurin, Zulfat Miftahutdinov

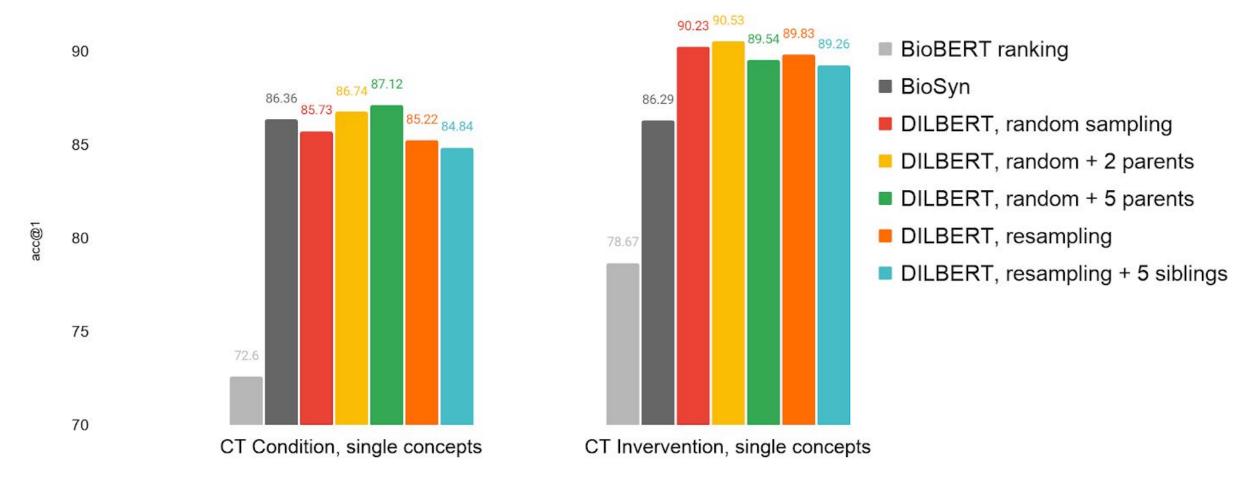
- Evaluation of benchmarks: BioCreative V CDR,
 BioCreative II GN, NCBI Disease, and TAC 2017 ADR
- App. 80% entity mentions in the test set are textual duplicates of other entities presented in the test set or train+dev sets
- Divergence in performance between these the original and refined test sets (app. 15%)
- Propose cross-terminology evaluation



https://www.aclweb.org/anthology/2020.coling-main.588.pdf

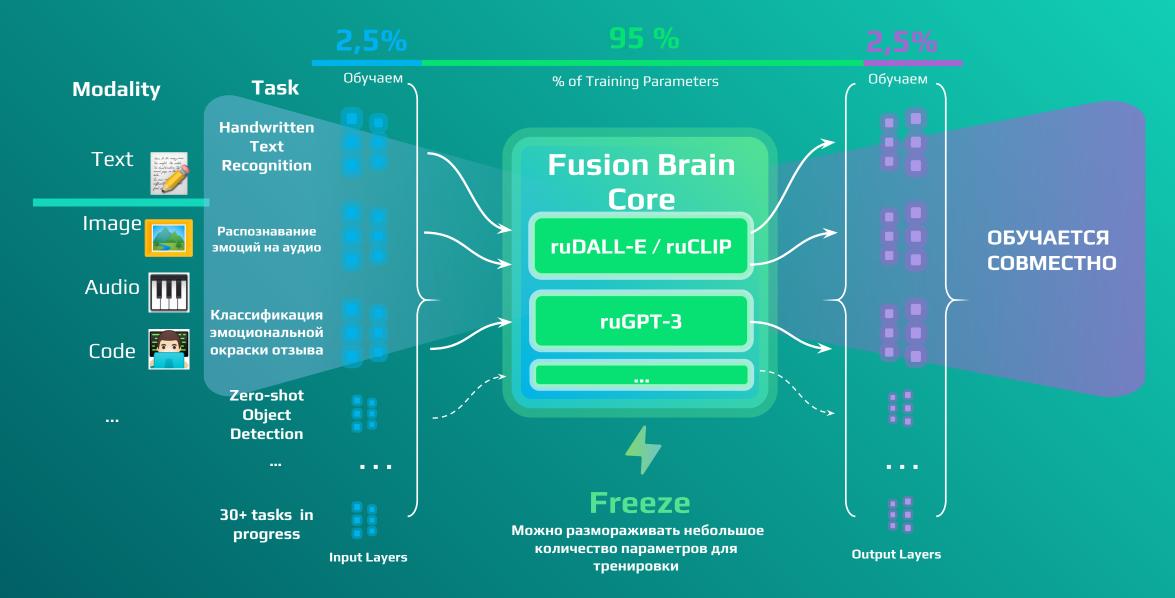


Experiments





Fusion Brain: Effective Multi-modal Multi-task model



https://github.com/sberbank-ai/fusion_brain_aij2021

