



**Glasgow Computational Biology Conference 2025** 

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# Accelerating Cross-Encoders for Biomedical Entity Linking

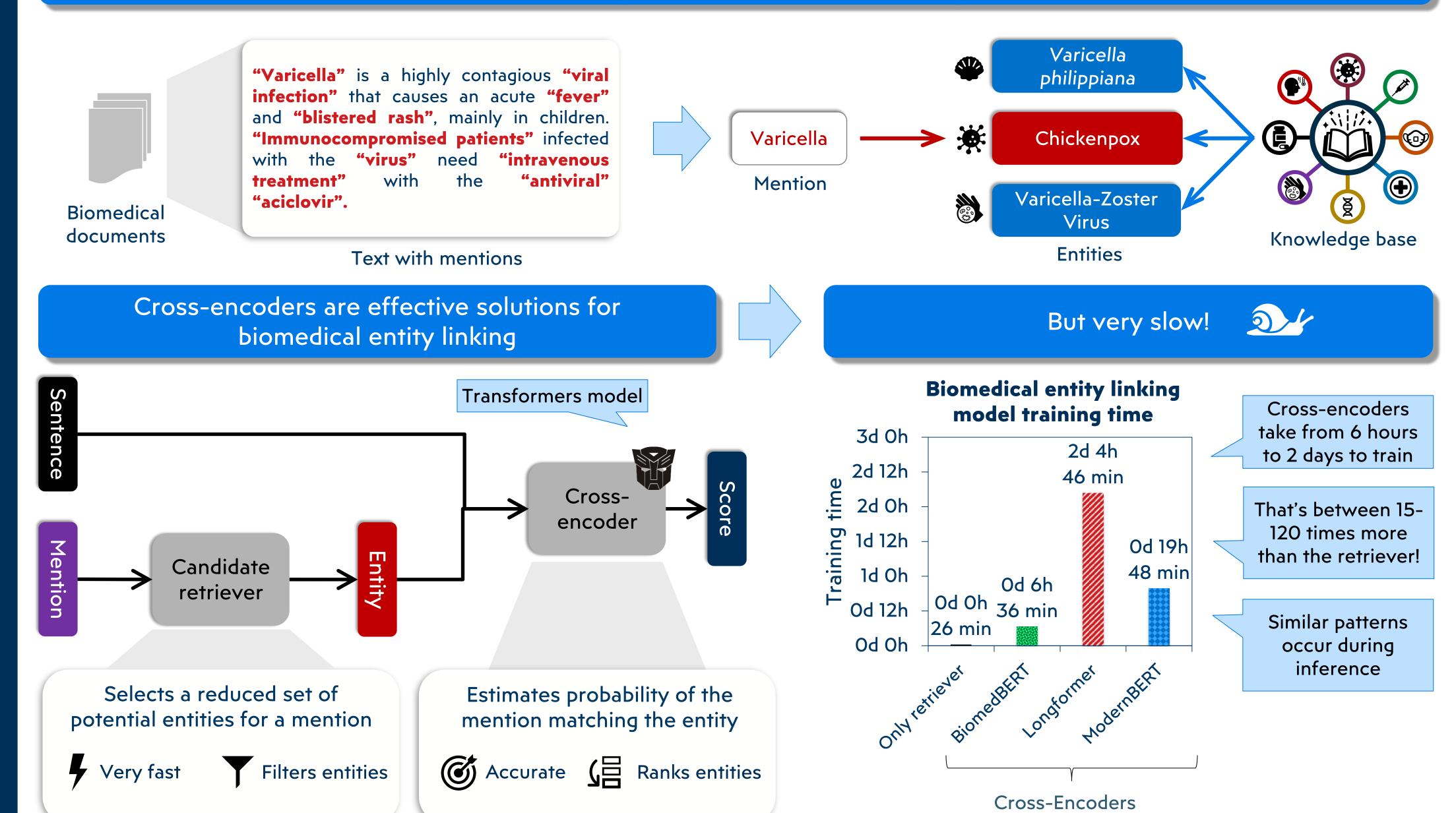
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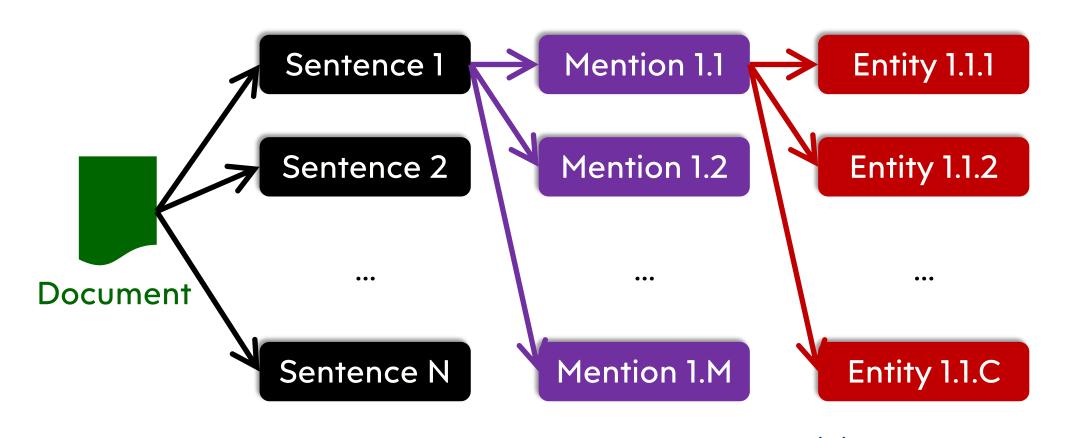
Full text

Biomedical entity linking matches mentions of biomedical concepts (diseases, chemicals) in text with unique entities within a knowledge base



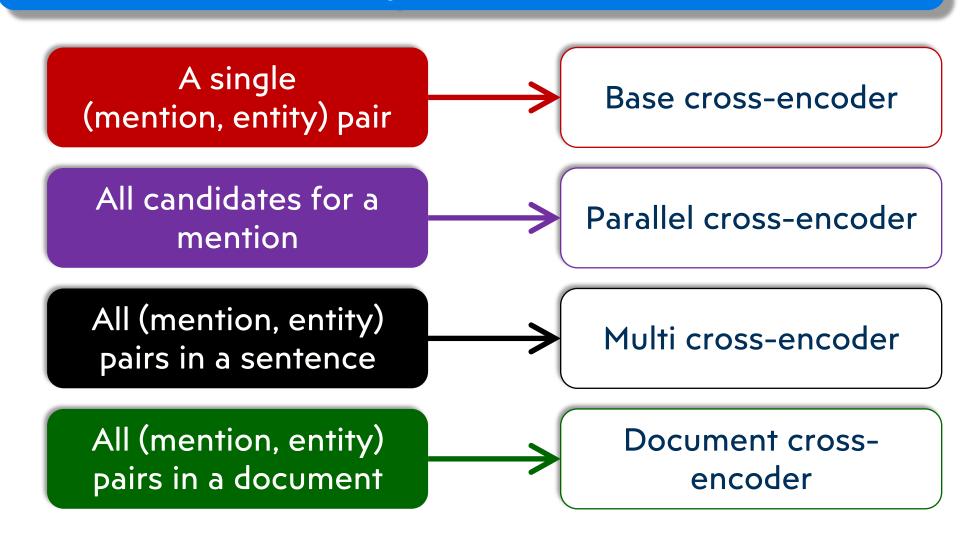
### Can we accelerate cross-encoders without losing accuracy?

Every time we use the cross-encoder, we only provide as input a single (mention, entity) pair



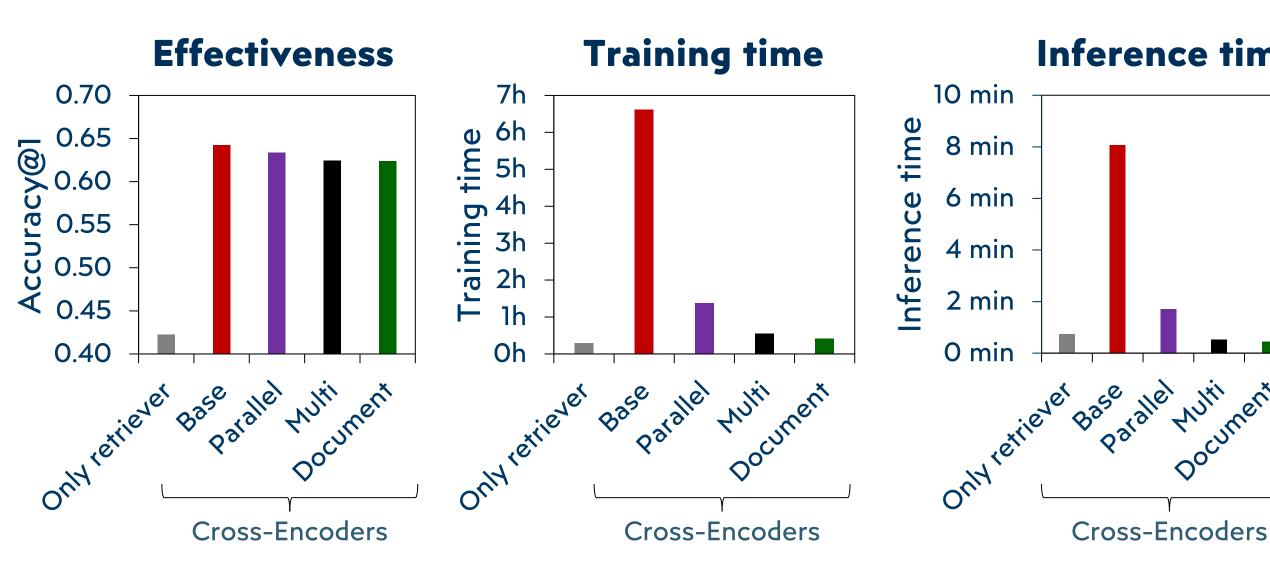
We are calling a cross-encoder multiple times for (a) the same mention, (b) the same sentence and (c) the same document

What if we show multiple (mention, entity) pairs simultaneously to the cross-encoder?



## Experiment

We evaluate the different BiomedBERT cross-encoders on the Medmentions dataset (more datasets and Transformers models in the paper)



# Inference time Parallel MITTER

### Conclusions

Processing more (mention, entity) pairs simultaneously has the following effects

Small variations on accuracy -3.42 to 2.76% differences with base model

Major improvements in training speed 2.68x – 36.97x faster training than base model

Major improvements in inference speed 3.8x - 26.47x faster inference than base model

Our solution is suitable on environments where speed is crucial