"Heavy-Light Chain Pair Identification in Antibodies using BERT (work title)"

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Abstract

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Glossary

Word Embeddings Mapping of words into vectors with real numbers.

1. Introduction

- 1.1. Background
- 1.2. Objectives
- 1.3. Scope of the Topic
- 1.4. Research Question
- 1.5. Nature of the Thesis
- 1.6. Relevance of the Thesis

2. Literature Review (work title)

2.1. Introduction to Antibodies

Antibodies are Y-shaped proteins that consist of two identical light chains (LCs) and two identical heavy chains (HCs) (Chiu, Goulet, Teplyakov, & Gilliland, 2019).

2.2. Antibody Engineering and Therapeutic Applications

2.3. Deep Learning Methods for Antibodies

Deep learning is a branch of machine learning that focuses on algorithms capable of identifying complex patterns in data by transforming low-level inputs (like pixels in an image) into high-level features (such as object shapes). It utilizes artificial neural networks (ANNs) with multiple layers between the input and output, making them "deep". These networks consist of nodes, or neurons, that process inputs and pass the outputs to subsequent layers, gradually extracting more abstract features. In the context of biochemistry, deep learning can start from basic data, like amino acid sequences, and learn to recognize complex biological structures or functions (Graves et al., 2020).

2.4. BERT and Transformers in Bioinformatics

BERT from Devlin, Chang, Lee, and Toutanova (2019) stands for "Bidirectional Encoder Representations from Transformers" and is based on a bidirectional language model. BERT uses the transformer according to Vaswani et al. (2017) as its architecture. At the time of publication, BERT was able to establish the state of the art in 11 natural language processing tasks (Devlin et al., 2019). The first forms of language modelling in connection with machine learning can be found in Mikolov, Chen, Corrado, and Dean (2013) in the form of the "skip-gram" model. In the skip-gram model, text or unlabelled data is used to train the probability distribution of the next word based on the previous words in the sentence. This process can then be used to calculate static word vectors, which serve as a starting point for other NLP tasks (Mikolov, Sutskever, Chen, Corrado, & Dean, 2013). The idea of this unidirectional language model was subsequently used by various other

publications and transferred to other architectures such as the Transformer according to Vaswani et al. (2017) (Radford, Narasimhan, Salimans, & Sutskever, 2018). In contrast to Radford et al. (2018), however, BERT uses a bidirectional language model. Figure 2.1 shows the structure of BERT with pretraining and fine-tuning in graphical form. The language model, or the step known as "pre-training", is trained using two tasks:

Masked language modelling: Since the words of the sentence are processed in parallel in the transformer architecture (Vaswani et al., 2017), individual words must be masked in bidirectional prediction. In the case of BERT, these are modelled with the

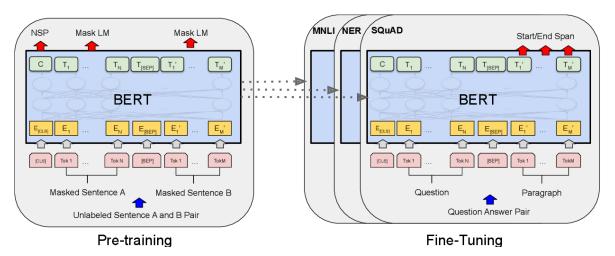


Figure 2.1.: BERT Overview (Devlin et al., 2019).

2.5. Heavy-Light Chain Pair Identification

2.5.1. Gap in the Literature

2.5.2. Conclusion

3. Materials & Methods

4. Results

5. Discussion

6. Conclusion

References

- Chiu, M. L., Goulet, D. R., Teplyakov, A., & Gilliland, G. L. (2019). Antibody structure and function: The basis for engineering therapeutics. *Antibodies*, 8(4). doi: 10.3390/antib8040055
- Devlin, J., Chang, M. W., Lee, K., & Toutanova, K. (2019). BERT: Pre-training of deep bidirectional transformers for language understanding. NAACL HLT 2019 2019 Conference of the North American Chapter of the Association for Computational Linguistics: Human Language Technologies Proceedings of the Conference, 1(Mlm), 4171–4186.
- Graves, J., Byerly, J., Priego, E., Makkapati, N., Parish, S. V., Medellin, B., & Berrondo, M. (2020). A Review of Deep Learning Methods for Antibodies. *Antibodies*, 9(2), 12. Retrieved from www.mdpi.com/journal/antibodies doi: 10.3390/antib9020012
- Mikolov, T., Chen, K., Corrado, G., & Dean, J. (2013). Efficient estimation of word representations in vector space. *1st International Conference on Learning Representations, ICLR 2013 Workshop Track Proceedings*, 1–12.
- Mikolov, T., Sutskever, I., Chen, K., Corrado, G., & Dean, J. (2013). Distributed representations of words and phrases and their compositionality. *Advances in Neural Information Processing Systems*, 1–9.
- Radford, A., Narasimhan, K., Salimans, T., & Sutskever, I. (2018). Improving Language Understanding by Generative Pre-Training. In *Openai*. Retrieved from https://api.semanticscholar.org/CorpusID:49313245
- Vaswani, A., Shazeer, N., Parmar, N., Uszkoreit, J., Jones, L., Gomez, A. N., ... Polosukhin, I. (2017). Attention is All you Need. In I. Guyon et al. (Eds.), Advances in neural information processing systems (Vol. 30). Curran Associates, Inc. Retrieved from https://proceedings.neurips.cc/paper{_}}files/paper/2017/file/3f5ee243547dee91fbd053c1c4a845aa-Paper.pdf

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A. Appendix

A.1. Link to the Code

The link to the entire code of this thesis can be found at: https://github.com/ibmm-unibe-ch/OAS_paired_sequences_cls.git

A.2. Declaration of Independence