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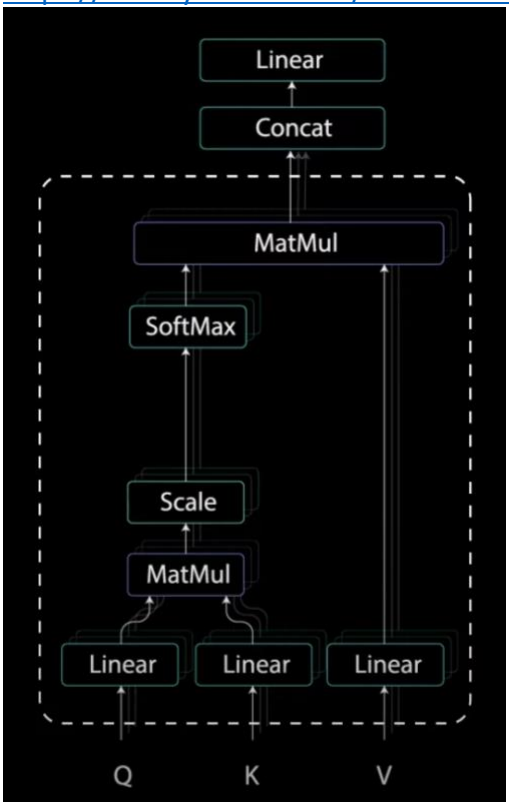
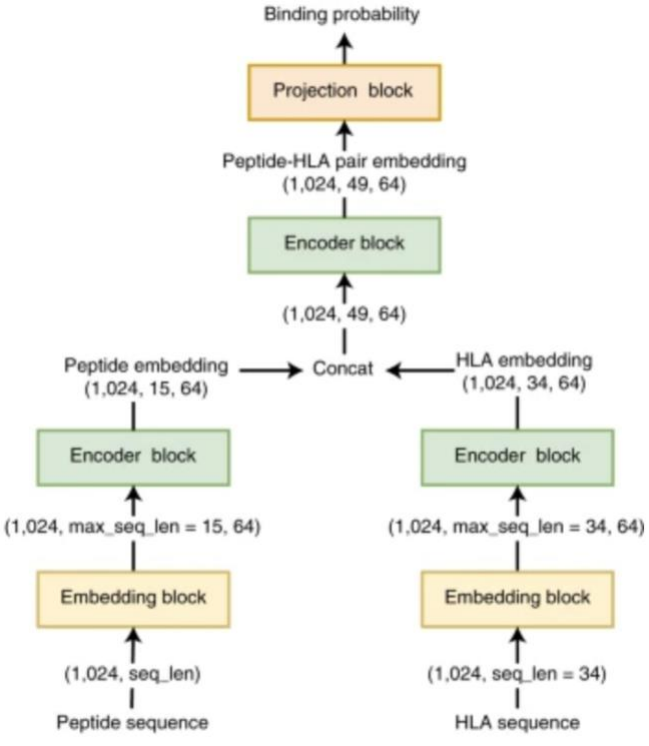
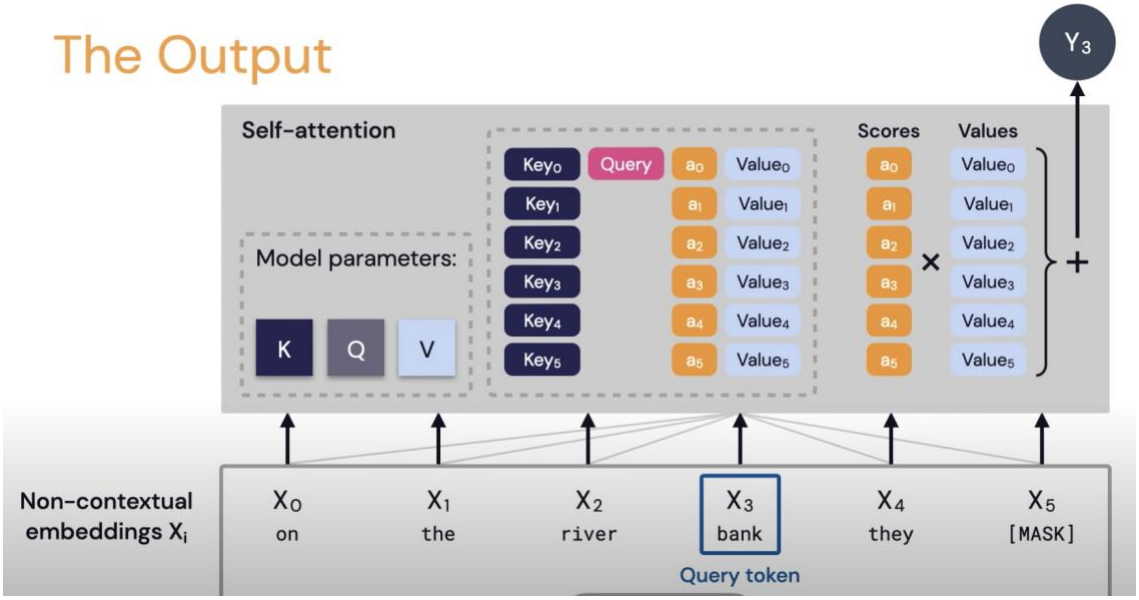
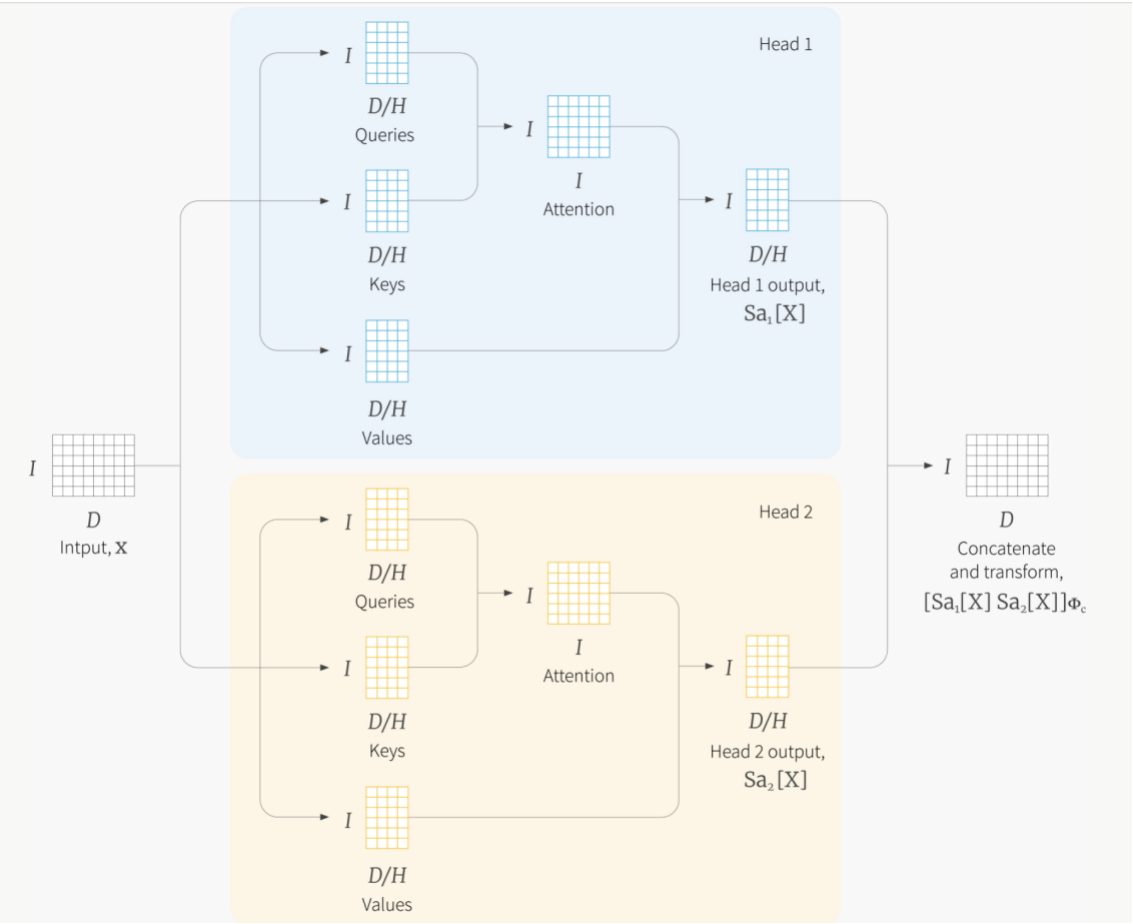


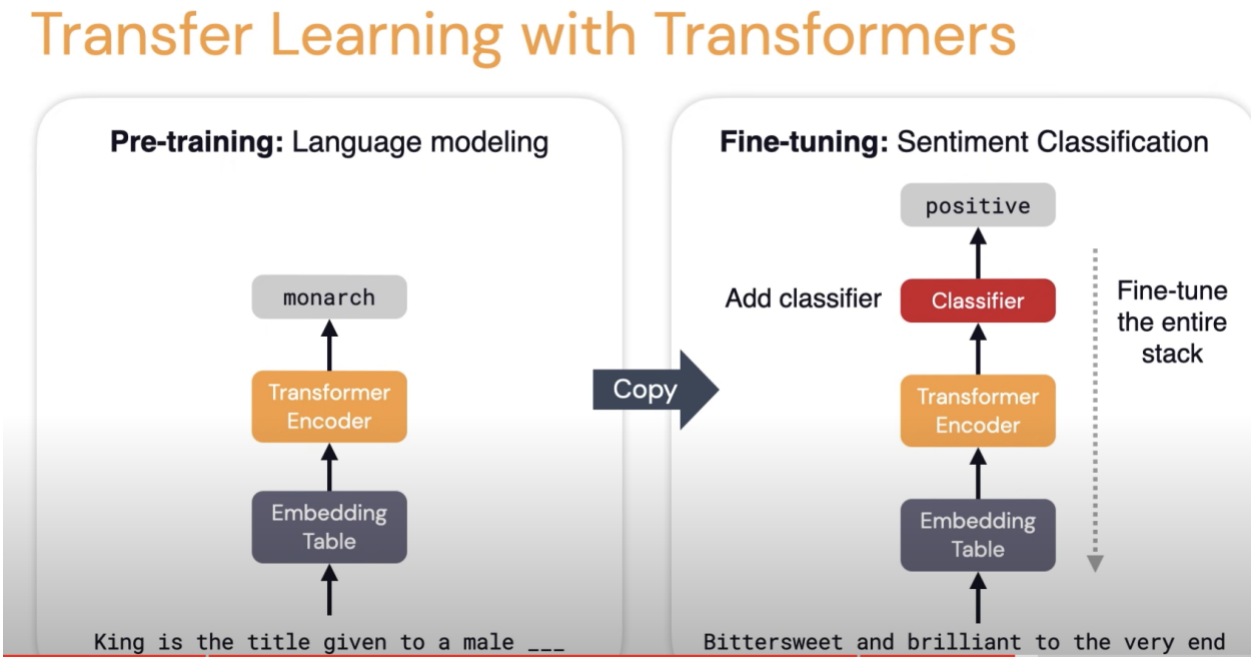


The TransPHLA model

https://www.youtube.com/watch?v=LE3NfEULV6k







Yumeng Zhang, Yangming Zhang, Yi Xiong, Hui Wang, Zixin Deng, Jiangning Song, Hong-Yu Ou, T4SEfinder: a bioinformatics tool for genome-scale prediction of bacterial type IV secreted effectors using pre-trained protein language model, *Briefings in Bioinformatics*, Volume 23, Issue 1, January 2022, bbab420, https://doi.org/10.1093/bib/bbab420

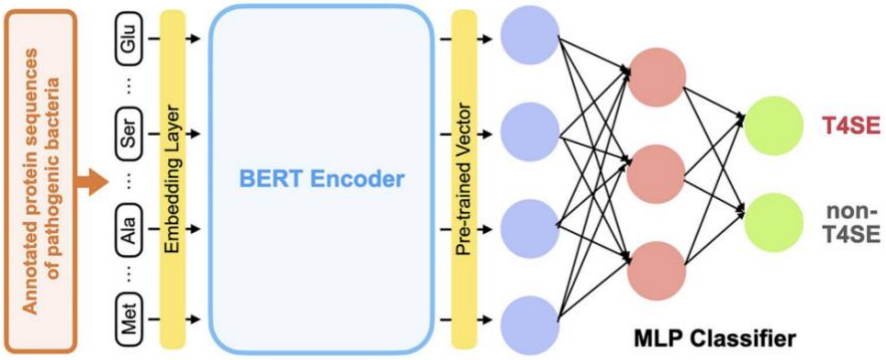


Figure 1. The model architecture of T4SEfinder (TAPEBert_MLP) to predict T4SEs. The TAPEBert_MLP model in T4SEfinder combines the TAPEBert pre-trained protein language model and a multi-layer perceptron (MLP) as the major architecture. The input of the model is protein sequences of arbitrary length that are composed of 20 common amino acids. The pre-trained BERT encoder is used to extract biological features, while MLP generates the final classification result.